

174282 mg

From: Seharaseyon, Jegatheesan
 Sent: Wednesday, December 14, 2005 5:15 PM
 To: STIC-Biotech/ChemLib
 Subject: Re: 10/084706

Hi,
 Please search SEQ ID NO: 2 of 10/084706.

Thanks.

J.Seharaseyon
 Art Unit 1647
 Remsen 4C61
 Mailbox 4C70
 Phone: (571)-272-0892
 Fax: (571)-273-0892

RECEIVED

DEC 15 2005

LCM/CHM, DIVISION
 (STIC)

 Searcher: _____
 Searcher Phone: _____
 Date Searcher Picked up: _____
 Date completed: _____
 Searcher Prep Time: _____
 Online Time: _____

 Type of Search
 NA# _____ AA# _____
 S/L: _____ Oligomer: _____
 Encode/Transl: _____
 Structure #: _____ Text: _____
 Inventor: _____ Litigation: _____

 Vendors and cost where applicable
 STN: _____
 DIALOG: _____
 QUESTEL/ORBIT: _____
 LEXIS/NEXIS: _____
 SEQUENCE SYSTEM: _____
 WWW/Internet: _____
 Other (Specify): _____

THIS PAGE BLANK (USPTO)

Protein Sequence Searches - February 2005

All of the sequence databases on ABSS have recently been updated.

- Please note that the curators of the UniProt database have purged some temporary accession numbers from the most recent version of UniProt. These sequences have been assigned new permanent accession numbers. The new UniProt record may not contain the previous temporary accession number.
- If you encounter an accession number from an older search run against UniProt (results file extension **.rup**) that can no longer be found in the database, the permanent record with the new accession number can be found by searching the old accession number in the UniProt Protein Archive database (UniPARC) at:

<http://www.pir.uniprot.org/database/archive.shtml>

If you have any questions regarding this information or your results, please contact any STIC searcher.

When submitting sequence search results for scanning into IFW, please include a copy of this attachment to assist any future Examiners or members of the public who may encounter UniProt temporary accession numbers.

THIS PAGE BLANK (USPTO)

Result	No.	Score	Query	Length	DB	ID	Description
1	1	874	100.0	187	1	IFNB_HUMAN	P01574 homo sapien
	2	874	100.0	187	2	Q5WVCG_HUMAN	Q5WVCG9 homo sapien
	3	832	95.2	187	1	IFNB_MACRA	Q77812 macaca fasciata
	4	827	94.6	187	2	Q15943_HUMAN	Q15943 homo sapien
	5	535	61.3	186	2	Q29412_PIG	Q29412 sus scrofa
	6	534.5	61.2	186	2	Q68104_PIG	Q68104 sus scrofa
	7	522.5	59.8	186	1	IFNB_FELCA	Q3n2J0 felis silvestris catus
	8	492.5	56.4	186	1	IFNB_BOVIN	P01576 bos taurus
	9	487.5	55.8	186	1	IFNB_HORSE	P05012 equus caballus
	10	458.5	52.5	186	1	IFNB_BOVIN	P01577 bos taurus
	11	440.5	50.4	186	1	IFNB_BOVIN	P01578 bos taurus
	12	342.5	39.2	182	1	IFNB_MOUSE	P01575 mus musculus
	13	335.5	38.4	184	1	IFNB_RAT	P70499 rattus norvegicus
	14	308	35.2	183	2	Q7YRX6_MACEU	Q7YRX6 macroceps eu
	15	301	34.4	187	2	Q6XW6_MACEU	Q7YRX8 macroceps eu
	16	289	33.1	183	2	Q7YRX8_MACEU	P05002 equus caballus
	17	289	33.1	195	1	IFNB_HORSE	Q7YRX7 macroceps eu
	18	278	31.8	183	2	Q7YRX7_MACEU	P05001 equus caballus
	19	268	30.7	195	1	IFNT_CEREL	O46633 cervus elaphus
	20	265.5	30.4	195	1	Q9CL5_BOVIN	Q9CL5 bos taurus
	21	265.5	30.4	195	1	Q86WN2_HUMAN	Q86WN2 homo sapiens
	22	264.5	30.3	208	2	Q14618_HUMAN	P05003 equus caballus
	23	264	30.2	184	1	IFNA1_HORSE	P05005 equus caballus
	24	264	30.2	184	1	IFNA2_HORSE	P05006 equus caballus
	25	264	30.2	184	1	IFNA4_HORSE	P051827 equus caballus
	26	262.5	30.0	195	2	Q5IS27_BOVCF	P05015 equus caballus
	27	260.5	29.8	189	1	IFNA5_HUMAN	P051618 homo sapiens
	28	260.5	29.8	189	2	Q5VW12_HUMAN	P05004 equus caballus
	29	260.5	29.8	189	1	IFNA2_HORSE	P051828 bubalus bubalis
	30	258.5	29.7	184	1	Q5IS28_BUBBU	
	31	258.5	29.6	195	2	Q5IS28_BUBBU	

RESULT 1							
IFNB_HUMAN				STANDARD:			
ID : IFNB_HUMAN				PRT; 187 AA.			
AC : P01574;				RN			
DT : 21-JUL-1986 (Rel. 01, Created)				RP			
DT : 21-JUL-1986 (Rel. 01, Last sequence update)				RN			
DT : 10-MAY-2005 (Rel. 47, Last annotation update)				RN			
DE : Interferon beta precursor (IFN-beta) (Fibroblast interferon).				RN			
GN : Name=IFNB1; Synonyms=IFB, IFNB;				RN			
OS : Homo sapiens (Human);				RN			
OC : Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominoidea;				RN			
OC : Homo.				RN			
OC : NCBI TaxID=9606;				RN			
RN : [1] _NUCLEOTIDE SEQUENCE.				RN			
RN : [2] _NUCLEOTIDE SEQUENCE.				RN			
RN : [3] _NUCLEOTIDE SEQUENCE.				RN			
RN : [4] _NUCLEOTIDE SEQUENCE.				RN			
RN : [5] _NUCLEOTIDE SEQUENCE.				RN			
RN : [6] _NUCLEOTIDE SEQUENCE.				RN			
RN : [7] _NUCLEOTIDE SEQUENCE.				RN			
RN : [8] _NUCLEOTIDE SEQUENCE.				RN			
RN : [9] _NUCLEOTIDE SEQUENCE.				RN			
RN : [10] _NUCLEOTIDE SEQUENCE.				RN			
RN : [11] _NUCLEOTIDE SEQUENCE.				RN			
RN : [12] _NUCLEOTIDE SEQUENCE.				RN			
RN : [13] _NUCLEOTIDE SEQUENCE.				RN			
RN : [14] _NUCLEOTIDE SEQUENCE.				RN			
RN : [15] _NUCLEOTIDE SEQUENCE.				RN			
RN : [16] _NUCLEOTIDE SEQUENCE.				RN			
RN : [17] _NUCLEOTIDE SEQUENCE.				RN			
RN : [18] _NUCLEOTIDE SEQUENCE.				RN			
RN : [19] _NUCLEOTIDE SEQUENCE.				RN			
RN : [20] _NUCLEOTIDE SEQUENCE.				RN			
RN : [21] _NUCLEOTIDE SEQUENCE.				RN			
RN : [22] _NUCLEOTIDE SEQUENCE.				RN			
RN : [23] _NUCLEOTIDE SEQUENCE.				RN			
RN : [24] _NUCLEOTIDE SEQUENCE.				RN			
RN : [25] _NUCLEOTIDE SEQUENCE.				RN			
RN : [26] _NUCLEOTIDE SEQUENCE.				RN			
RN : [27] _NUCLEOTIDE SEQUENCE.				RN			
RN : [28] _NUCLEOTIDE SEQUENCE.				RN			
RN : [29] _NUCLEOTIDE SEQUENCE.				RN			
RN : [30] _NUCLEOTIDE SEQUENCE.				RN			
RN : [31] _NUCLEOTIDE SEQUENCE.				RN			
RN : [32] _NUCLEOTIDE SEQUENCE.				RN			
RN : [33] _NUCLEOTIDE SEQUENCE.				RN			
RN : [34] _NUCLEOTIDE SEQUENCE.				RN			
RN : [35] _NUCLEOTIDE SEQUENCE.				RN			
RN : [36] _NUCLEOTIDE SEQUENCE.				RN			
RN : [37] _NUCLEOTIDE SEQUENCE.				RN			
RN : [38] _NUCLEOTIDE SEQUENCE.				RN			
RN : [39] _NUCLEOTIDE SEQUENCE.				RN			
RN : [40] _NUCLEOTIDE SEQUENCE.				RN			
RN : [41] _NUCLEOTIDE SEQUENCE.				RN			
RN : [42] _NUCLEOTIDE SEQUENCE.				RN			
RN : [43] _NUCLEOTIDE SEQUENCE.				RN			
RN : [44] _NUCLEOTIDE SEQUENCE.				RN			
RN : [45] _NUCLEOTIDE SEQUENCE.				RN			
RN : [46] _NUCLEOTIDE SEQUENCE.				RN			
RN : [47] _NUCLEOTIDE SEQUENCE.				RN			
RN : [48] _NUCLEOTIDE SEQUENCE.				RN			
RN : [49] _NUCLEOTIDE SEQUENCE.				RN			
RN : [50] _NUCLEOTIDE SEQUENCE.				RN			
RN : [51] _NUCLEOTIDE SEQUENCE.				RN			
RN : [52] _NUCLEOTIDE SEQUENCE.				RN			
RN : [53] _NUCLEOTIDE SEQUENCE.				RN			
RN : [54] _NUCLEOTIDE SEQUENCE.				RN			
RN : [55] _NUCLEOTIDE SEQUENCE.				RN			
RN : [56] _NUCLEOTIDE SEQUENCE.				RN			
RN : [57] _NUCLEOTIDE SEQUENCE.				RN			
RN : [58] _NUCLEOTIDE SEQUENCE.				RN			
RN : [59] _NUCLEOTIDE SEQUENCE.				RN			
RN : [60] _NUCLEOTIDE SEQUENCE.				RN			
RN : [61] _NUCLEOTIDE SEQUENCE.				RN			
RN : [62] _NUCLEOTIDE SEQUENCE.				RN			
RN : [63] _NUCLEOTIDE SEQUENCE.				RN			
RN : [64] _NUCLEOTIDE SEQUENCE.				RN			
RN : [65] _NUCLEOTIDE SEQUENCE.				RN			
RN : [66] _NUCLEOTIDE SEQUENCE.				RN			
RN : [67] _NUCLEOTIDE SEQUENCE.				RN			
RN : [68] _NUCLEOTIDE SEQUENCE.				RN			
RN : [69] _NUCLEOTIDE SEQUENCE.				RN			
RN : [70] _NUCLEOTIDE SEQUENCE.				RN			
RN : [71] _NUCLEOTIDE SEQUENCE.				RN			
RN : [72] _NUCLEOTIDE SEQUENCE.				RN			
RN : [73] _NUCLEOTIDE SEQUENCE.				RN			
RN : [74] _NUCLEOTIDE SEQUENCE.				RN			
RN : [75] _NUCLEOTIDE SEQUENCE.				RN			

"Synthesis of human fibroblast interferon by *E. coli.*".
 RT RL Nucleic Acids Res. 8:4057-4074(1980).
 RN [7]
 NUCLEOTIDE SEQUENCE.
 RP MEDLINE=86035565; PubMed=2414376;
 RX MAY L.T., Gehgal P.B.;
 RA "On the relationship between human interferon alpha 1 and beta 1 genes";
 RT J. Interferon Res. 5:521-526 (1985).
 RN [8]
 NUCLEOTIDE SEQUENCE [LARGE SCALE mRNA]
 RP MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RX Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klaunzer R.D., Collins F.S., Wagner L., Scheuer C.M., Schuler G.D.,
 RA Altschul S.F., Zelberg B., Buetow K.H., Shneifer C.P., Bhac N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soresi M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
 RA Bosak S.A., McEwan P.J., McKeran K.J., Malek J.A., Gunnarath P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakley R.W., Touchman J.W., Greenz J.M., Myers R.M.,
 RA Rodriguez A.C., Grinblat J., Schmutz J., Krzywinski M.I., Skalska U., Smailus D.E.,
 RA Butterfield Y.S.N., Jones S.J.M., Marra M.A.;
 RA Schnarch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
 RN [9]
 NUCLEOTIDE SEQUENCE OF 1-68.
 RP MEDLINE=81053854; PubMed=6159597;
 RX Houghton M., Stewart A.G.-Doel S.M., Emtage J.S., Eaton M.A.W.,
 RA Smith J.C., Patel T.P., Lewis H.M., Porter A.G., Birch J.R.,
 RA Cartwright T., Carey N.H.;
 RT "The amino-terminal sequence of human fibroblast interferon as deduced
 RT from reverse transcripts obtained using synthetic oligonucleotide
 RT primers";
 RL Nucleic Acids Res. 8:1913-1931(1980).
 RN [10]
 RP DISULFIDE BOND.
 RX MEDLINE=811223083; PubMed=6162107;
 RA Wetzell R.;
 RT "Assignment of the disulphide bonds of leukocyte interferon.";
 RL Nature 289:606-607 (1981).
 RN [11]
 NUCLEOTIDE SEQUENCE OF 71-187 (VARIANT CLONE PF526).
 RP MEDLINE=82080683; PubMed=6171735;
 RX Shepard H.M., Leung D., Stebbing N., Goeddel D.V.;
 RT "A single amino acid change in IFN-beta1 abolishes its antiviral
 activity";
 RL Nature 294:5563-565 (1981).
 RN [12]
 RP X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS).
 RX MEDLINE=98004451; PubMed=9342220; DOI=10.1073/pnas.94.22.11813;
 RA Karpusas M., Nolte M., Benton C.B., Meier W., Lipcomb W.N., Goetz S.;
 RT "The crystal structure of human interferon beta at 2.2-A resolution.";
 RL Proc. Natl. Acad. Sci. U.S.A. 94:11813-11818 (1997);
 CC "-";
 RT FUNCTION: Has antiviral, antibacterial and anticancer activities.
 RL SUBUNIT: Monomer.
 CC "-";
 CC SUBCELLULAR LOCATION: Secreted.
 CC "-";
 CC PHARMACEUTICAL: Available under the names Avonex (Biogen),
 Betaseron (Berlex) and Rebif (Serono). Used in the treatment of
 multiple sclerosis (MS). Betaseron is a slightly modified form of
 IFNB1 with two residue substitutions.
 CC "-";
 CC SIMILARITY: Belongs to the alpha/beta interferon family.
 CC "-";
 CC DATABASE: NAME=Avonex; NOTE=Clinical information on Avonex;
 CC WWW="http://www.msvaproject/avonex.portal".
 CC "-";
 CC DATABASE: NAME=Betaseron; NOTE=Clinical information on Betaseron;
 CC WWW="http://www.betaseron.com/betas/index.jsp".
 DB

This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL Outstation - European Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not removed.

CC DR EMBL; V00534; CAA23795_1; -; Genomic_DNA.
 CC DR EMBL; V00535; CAA23796_1; -; Genomic_C_DNA.
 CC DR EMBL; V00546; CAA23807_1; -; mRNA.
 CC DR EMBL; V00547; CAA23808_1; -; mRNA.
 CC DR EMBL; BC069314; AAH69314_1; -; mRNA.
 CC DR EMBL; M28622; AAA36040_1; -; mRNA.
 CC DR PIR: A93721; IVHUB1.
 CC DR PDB; 1AUL; X-RAY; A/B=22-187.
 CC DR Ensembl; ENSG0000171855; Homo_sapiens.
 CC DR HGNC; 5434; IFNB1.
 CC DR MIM; 147540; -.
 CC DR GO:0005576; C:extracellular region; IC.
 CC DR GO:0005132; P:interferon-alpha/beta receptor binding; NAS.
 CC DR GO:0003036; P:anti-inflammatory response; NAS.
 CC DR GO:0042100; P:B cell proliferation; NAS.
 CC DR GO:0006919; P:caspase activation; NAS.
 CC DR GO:0007166; P:cell surface receptor linked signal transdu...; TAS.
 CC DR GO:0030101; P:natural killer cell activation; NAS.
 CC DR GO:0008285; P:negative regulation of cell proliferation; NAS.
 CC DR GO:0046597; P:negative regulation of virion penetration; NAS.
 CC DR GO:0045089; P:positive regulation of innate immune response; NAS.
 CC DR GO:0045343; P:regulation of MHC Class I biosynthesis; NAS.
 CC DR GO:0009615; P:response to virus; NAS.
 CC DR Interpro; IPR00471; Interferon_abd.
 CC DR PANTHER; PTHR11691; Interferon_abd; 1.
 CC DR Pfam; PF00143; Interferon; 1.
 CC DR PRINTS; PR00266; INTERFERON_AB.
 CC DR ProDom; PD00050; Interferon_abd; 1.
 CC DR PROSITE; PS00052; INTERFERON_A_B_D; 1.
 CC KW 3D-structure; Antiviral defense; Cytokine; Glycoprotein;
 CC KW Pharmaceutical; Signal.
 FT SIGNAL; 1
 FT PT CHAIN; 22 187
 FT PT CARBOHYD; 101 101
 FT PT DISULFID; 52 162
 FT PT VARIANT; 162 162
 FT PT TURN; 183 184
 FT SQ SEQUENCE; 187 AA; 22294 MW; OB013D4087723CEC CRC64;
 FT PT HELIX; 24 44
 FT PT HELIX; 63 66
 FT PT HELIX; 73 92
 FT PT TURN; 96 97
 FT PT HELIX; 102 125
 FT PT TURN; 126 128
 FT PT HELIX; 134 156
 FT PT TURN; 157 159
 FT PT HELIX; 161 182
 FT PT TURN; 183 184
 FT SQ SEQUENCE; 187 AA; 22294 MW; OB013D4087723CEC CRC64;
 FT PT HELIX; 24 44
 FT PT HELIX; 63 66
 FT PT HELIX; 73 92
 FT PT TURN; 96 97
 FT PT HELIX; 102 125
 FT PT TURN; 126 128
 FT PT HELIX; 134 156
 FT PT TURN; 157 159
 FT PT HELIX; 161 182
 FT PT TURN; 183 184
 FT SQ SEQUENCE; 187 AA; 22294 MW; OB013D4087723CEC CRC64;
 FT PT HELIX; 24 44
 FT PT HELIX; 63 66
 FT PT HELIX; 73 92
 FT PT TURN; 96 97
 FT PT HELIX; 102 125
 FT PT TURN; 126 128
 FT PT HELIX; 134 156
 FT PT TURN; 157 159
 FT PT HELIX; 161 182
 FT PT TURN; 183 184
 FT SQ SEQUENCE; 187 AA; 22294 MW; OB013D4087723CEC CRC64;
 FT PT HELIX; 24 44
 FT PT HELIX; 63 66
 FT PT HELIX; 73 92
 FT PT TURN; 96 97
 FT PT HELIX; 102 125
 FT PT TURN; 126 128
 FT PT HELIX; 134 156
 FT PT TURN; 157 159
 FT PT HELIX; 161 182
 FT PT TURN; 183 184
 FT SQ SEQUENCE; 187 AA; 22294 MW; OB013D4087723CEC CRC64;
 FT PT HELIX; 24 44
 FT PT HELIX; 63 66
 FT PT HELIX; 73 92
 FT PT TURN; 96 97
 FT PT HELIX; 102 125
 FT PT TURN; 126 128
 FT PT HELIX; 134 156
 FT PT TURN; 157 159
 FT PT HELIX; 161 182
 FT PT TURN; 183 184
 FT SQ SEQUENCE; 187 AA; 22294 MW; OB013D4087723CEC CRC64;
 FT PT HELIX; 24 44
 FT PT HELIX; 63 66
 FT PT HELIX; 73 92
 FT PT TURN; 96 97
 FT PT HELIX; 102 125
 FT PT TURN; 126 128
 FT PT HELIX; 134 156
 FT PT TURN; 157 159
 FT PT HELIX; 161 182
 FT PT TURN; 183 184
 FT SQ SEQUENCE; 187 AA; 22294 MW; OB013D4087723CEC CRC64;
 FT PT HELIX; 24 44
 FT PT HELIX; 63 66
 FT PT HELIX; 73 92
 FT PT TURN; 96 97
 FT PT HELIX; 102 125
 FT PT TURN; 126 128
 FT PT HELIX; 134 156
 FT PT TURN; 157 159
 FT PT HELIX; 161 182
 FT PT TURN; 183 184
 FT SQ SEQUENCE; 187 AA; 22294 MW; OB013D4087723CEC CRC64;
 FT PT HELIX; 24 44
 FT PT HELIX; 63 66
 FT PT HELIX; 73 92
 FT PT TURN; 96 97
 FT PT HELIX; 102 125
 FT PT TURN; 126 128
 FT PT HELIX; 134 156
 FT PT TURN; 157 159
 FT PT HELIX; 161 182
 FT PT TURN; 183 184
 FT SQ SEQUENCE; 187 AA; 22294 MW; OB013D4087723CEC CRC64;
 FT PT HELIX; 24 44
 FT PT HELIX; 63 66
 FT PT HELIX; 73 92
 FT PT TURN; 96 97
 FT PT HELIX; 102 125
 FT PT TURN; 126 128
 FT PT HELIX; 134 156
 FT PT TURN; 157 159
 FT PT HELIX; 161 182
 FT PT TURN; 183 184
 FT SQ SEQUENCE; 187 AA; 22294 MW; OB013D4087723CEC CRC64;
 FT PT HELIX; 24 44
 FT PT HELIX; 63 66
 FT PT HELIX; 73 92
 FT PT TURN; 96 97
 FT PT HELIX; 102 125
 FT PT TURN; 126 128
 FT PT HELIX; 134 156
 FT PT TURN; 157 159
 FT PT HELIX; 161 182
 FT PT TURN; 183 184
 FT SQ SEQUENCE; 187 AA; 22294 MW; OB013D4087723CEC CRC64;
 FT PT HELIX; 24 44
 FT PT HELIX; 63 66
 FT PT HELIX; 73 92
 FT PT TURN; 96 97
 FT PT HELIX; 102 125
 FT PT TURN; 126 128
 FT PT HELIX; 134 156
 FT PT TURN; 157 159
 FT PT HELIX; 161 182
 FT PT TURN; 183 184
 FT SQ SEQUENCE; 187 AA; 22294 MW; OB013D4087723CEC CRC64;
 FT PT HELIX; 24 44
 FT PT HELIX; 63 66
 FT PT HELIX; 73 92
 FT PT TURN; 96 97
 FT PT HELIX; 102 125
 FT PT TURN; 126 128
 FT PT HELIX; 134 156
 FT PT TURN; 157 159
 FT PT HELIX; 161 182
 FT PT TURN; 183 184
 FT SQ SEQUENCE; 187 AA; 22294 MW; OB013D4087723CEC CRC64;
 FT PT HELIX; 24 44
 FT PT HELIX; 63 66
 FT PT HELIX; 73 92
 FT PT TURN; 96 97
 FT PT HELIX; 102 125
 FT PT TURN; 126 128
 FT PT HELIX; 134 156
 FT PT TURN; 157 159
 FT PT HELIX; 161 182
 FT PT TURN; 183 184
 FT SQ SEQUENCE; 187 AA; 22294 MW; OB013D4087723CEC CRC64;
 FT PT HELIX; 24 44
 FT PT HELIX; 63 66
 FT PT HELIX; 73 92
 FT PT TURN; 96 97
 FT PT HELIX; 102 125
 FT PT TURN; 126 128
 FT PT HELIX; 134 156
 FT PT TURN; 157 159
 FT PT HELIX; 161 182
 FT PT TURN; 183 184
 FT SQ SEQUENCE; 187 AA; 22294 MW; OB013D4087723CEC CRC64;
 FT PT HELIX; 24 44
 FT PT HELIX; 63 66
 FT PT HELIX; 73 92
 FT PT TURN; 96 97
 FT PT HELIX; 102 125
 FT PT TURN; 126 128
 FT PT HELIX; 134 156
 FT PT TURN; 157 159
 FT PT HELIX; 161 182
 FT PT TURN; 183 184
 FT SQ SEQUENCE; 187 AA; 22294 MW; OB013D4087723CEC CRC64;
 FT PT HELIX; 24 44
 FT PT HELIX; 63 66
 FT PT HELIX; 73 92
 FT PT TURN; 96 97
 FT PT HELIX; 102 125
 FT PT TURN; 126 128
 FT PT HELIX; 134 156
 FT PT TURN; 157 159
 FT PT HELIX; 161 182
 FT PT TURN; 183 184
 FT SQ SEQUENCE; 187 AA; 22294 MW; OB013D4087723CEC CRC64;
 FT PT HELIX; 24 44
 FT PT HELIX; 63 66
 FT PT HELIX; 73 92
 FT PT TURN; 96 97
 FT PT HELIX; 102 125
 FT PT TURN; 126 128
 FT PT HELIX; 134 156
 FT PT TURN; 157 159
 FT PT HELIX; 161 182
 FT PT TURN; 183 184
 FT SQ SEQUENCE; 187 AA; 22294 MW; OB013D4087723CEC CRC64;
 FT PT HELIX; 24 44
 FT PT HELIX; 63 66
 FT PT HELIX; 73 92
 FT PT TURN; 96 97
 FT PT HELIX; 102 125
 FT PT TURN; 126 128
 FT PT HELIX; 134 156
 FT PT TURN; 157 159
 FT PT HELIX; 161 182
 FT PT TURN; 183 184
 FT SQ SEQUENCE; 187 AA; 22294 MW; OB013D4087723CEC CRC64;
 FT PT HELIX; 24 44
 FT PT HELIX; 63 66
 FT PT HELIX; 73 92
 FT PT TURN; 96 97
 FT PT HELIX; 102 125
 FT PT TURN; 126 128
 FT PT HELIX; 134 156
 FT PT TURN; 157 159
 FT PT HELIX; 161 182
 FT PT TURN; 183 184
 FT SQ SEQUENCE; 187 AA; 22294 MW; OB013D4087723CEC CRC64;
 FT PT HELIX; 24 44
 FT PT HELIX; 63 66
 FT PT HELIX; 73 92
 FT PT TURN; 96 97
 FT PT HELIX; 102 125
 FT PT TURN; 126 128
 FT PT HELIX; 134 156
 FT PT TURN; 157 159
 FT PT HELIX; 161 182
 FT PT TURN; 183 184
 FT SQ SEQUENCE; 187 AA; 22294 MW; OB013D4087723CEC CRC64;
 FT PT HELIX; 24 44
 FT PT HELIX; 63 66
 FT PT HELIX; 73 92
 FT PT TURN; 96 97
 FT PT HELIX; 102 125
 FT PT TURN; 126 128
 FT PT HELIX; 134 156
 FT PT TURN; 157 159
 FT PT HELIX; 161 182
 FT PT TURN; 183 184
 FT SQ SEQUENCE; 187 AA; 22294 MW; OB013D4087723CEC CRC64;
 FT PT HELIX; 24 44
 FT PT HELIX; 63 66
 FT PT HELIX; 73 92
 FT PT TURN; 96 97
 FT PT HELIX; 102 125
 FT PT TURN; 126 128
 FT PT HELIX; 134 156
 FT PT TURN; 157 159
 FT PT HELIX; 161 182
 FT PT TURN; 183 184
 FT SQ SEQUENCE; 187 AA; 22294 MW; OB013D4087723CEC CRC64;
 FT PT HELIX; 24 44
 FT PT HELIX; 63 66
 FT PT HELIX; 73 92
 FT PT TURN; 96 97
 FT PT HELIX; 102 125
 FT PT TURN; 126 128
 FT PT HELIX; 134 156
 FT PT TURN; 157 159
 FT PT HELIX; 161 182
 FT PT TURN; 183 184
 FT SQ SEQUENCE; 187 AA; 22294 MW; OB013D4087723CEC CRC64;
 FT PT HELIX; 24 44
 FT PT HELIX; 63 66
 FT PT HELIX; 73 92
 FT PT TURN; 96 97
 FT PT HELIX; 102 125
 FT PT TURN; 126 128
 FT PT HELIX; 134 156
 FT PT TURN; 157 159
 FT PT HELIX; 161 182
 FT PT TURN; 183 184
 FT SQ SEQUENCE; 187 AA; 22294 MW; OB013D4087723CEC CRC64;
 FT PT HELIX; 24 44
 FT PT HELIX; 63 66
 FT PT HELIX; 73 92
 FT PT TURN; 96 97
 FT PT HELIX; 102 125
 FT PT TURN; 126 128
 FT PT HELIX; 134 156
 FT PT TURN; 157 159
 FT PT HELIX; 161 182
 FT PT TURN; 183 184
 FT SQ SEQUENCE; 187 AA; 22294 MW; OB013D4087723CEC CRC64;
 FT PT HELIX; 24 44
 FT PT HELIX; 63 66
 FT PT HELIX; 73 92
 FT PT TURN; 96 97
 FT PT HELIX; 102 125
 FT PT TURN; 126 128
 FT PT HELIX; 134 156
 FT PT TURN; 157 159
 FT PT HELIX; 161 182
 FT PT TURN; 183 184
 FT SQ SEQUENCE; 187 AA; 22294 MW; OB013D4087723CEC CRC64;
 FT PT HELIX; 24 44
 FT PT HELIX; 63 66
 FT PT HELIX; 73 92
 FT PT TURN; 96 97
 FT PT HELIX; 102 125
 FT PT TURN; 126 128
 FT PT HELIX; 134 156
 FT PT TURN; 157 159
 FT PT HELIX; 161 182
 FT PT TURN; 183 184
 FT SQ SEQUENCE; 187 AA; 22294 MW; OB013D4087723CEC CRC64;
 FT PT HELIX; 24 44
 FT PT HELIX; 63 66
 FT PT HELIX; 73 92
 FT PT TURN; 96 97
 FT PT HELIX; 102 125
 FT PT TURN; 126 128
 FT PT HELIX; 134 156
 FT PT TURN; 157 159
 FT PT HELIX; 161 182
 FT PT TURN; 183 184
 FT SQ SEQUENCE; 187 AA; 22294 MW; OB013D4087723CEC CRC64;
 FT PT HELIX; 24 44
 FT PT HELIX; 63 66
 FT PT HELIX; 73 92
 FT PT TURN; 96 97
 FT PT HELIX; 102 125
 FT PT TURN; 126 128
 FT PT HELIX; 134 156
 FT PT TURN; 157 159
 FT PT HELIX; 161 182
 FT PT TURN; 183 184
 FT SQ SEQUENCE; 187 AA; 22294 MW; OB013D4087723CEC CRC64;
 FT PT HELIX; 24 44
 FT PT HELIX; 63 66
 FT PT HELIX; 73 92
 FT PT TURN; 96 97
 FT PT HELIX; 102 125
 FT PT TURN; 126 128
 FT PT HELIX; 134 156
 FT PT TURN; 157 159
 FT PT HELIX; 161 182
 FT PT TURN; 183 184
 FT SQ SEQUENCE; 187 AA; 22294 MW; OB013D4087723CEC CRC64;
 FT PT HELIX; 24 44
 FT PT HELIX; 63 66
 FT PT HELIX; 73 92
 FT PT TURN; 96 97
 FT PT HELIX; 102 125
 FT PT TURN; 126 128
 FT PT HELIX; 134 156
 FT PT TURN; 157 159
 FT PT HELIX; 161 182
 FT PT TURN; 183 184
 FT SQ SEQUENCE; 187 AA; 22294 MW; OB013D4087723CEC CRC64;
 FT PT HELIX; 24 44
 FT PT HELIX; 63 66
 FT PT HELIX; 73 92
 FT PT TURN; 96 97
 FT PT HELIX; 102 125
 FT PT TURN; 126 128
 FT PT HELIX; 134 156
 FT PT TURN; 157 159
 FT PT HELIX; 161 182
 FT PT TURN; 183 184
 FT SQ SEQUENCE; 187 AA; 22294 MW; OB013D4087723CEC CRC64;
 FT PT HELIX; 24 44
 FT PT HELIX; 63 66
 FT PT HELIX; 73 92
 FT PT TURN; 96 97
 FT PT HELIX; 102 125
 FT PT TURN; 126 128
 FT PT HELIX; 134 156
 FT PT TURN; 157 159
 FT PT HELIX; 161 182
 FT PT TURN; 183 184
 FT SQ SEQUENCE; 187 AA; 22294 MW; OB013D4087723CEC CRC64;
 FT PT HELIX; 24 44
 FT PT HELIX; 63 66
 FT PT HELIX; 73 92
 FT PT TURN; 96 97
 FT PT HELIX; 102 125
 FT PT TURN; 126 128
 FT PT HELIX; 134 156
 FT PT TURN; 157 159
 FT PT HELIX; 161 182
 FT PT TURN; 183 184
 FT SQ SEQUENCE; 187 AA; 22294 MW; OB013D4087723CEC CRC64;
 FT PT HELIX; 24 44
 FT PT HELIX; 63 66
 FT PT HELIX; 73 92
 FT PT TURN; 96 97
 FT PT HELIX; 102 125
 FT PT TURN; 126 128
 FT PT HELIX; 134 156
 FT PT TURN; 157 159
 FT PT HELIX; 161 182
 FT PT TURN; 183 184
 FT SQ SEQUENCE; 187 AA; 22294 MW; OB013D4087723CEC CRC64;
 FT PT HELIX; 24 44
 FT PT HELIX; 63 66
 FT PT HELIX; 73 92
 FT PT TURN; 96 97
 FT PT HELIX; 102 125
 FT PT TURN; 126 128
 FT PT HELIX; 134 156
 FT PT TURN; 157 159
 FT PT HELIX; 161 182
 FT PT TURN; 183 184
 FT SQ SEQUENCE; 187 AA; 22294 MW; OB013D4087723CEC CRC64;
 FT PT HELIX; 24 44
 FT PT HELIX; 63 66
 FT PT HELIX; 73 92
 FT PT TURN; 96 97
 FT PT HELIX; 102 125
 FT PT TURN; 126 128
 FT PT HELIX; 134 156
 FT PT TURN; 157 159
 FT PT HELIX; 161 182
 FT PT TURN; 183 184
 FT SQ SEQUENCE; 187 AA; 22294 MW; OB013D4087723CEC CRC64;
 FT PT HELIX; 24 44
 FT PT HELIX; 63 66
 FT PT HELIX; 73 92
 FT PT TURN; 96 97
 FT PT HELIX; 102 125
 FT PT TURN; 126 128
 FT PT HELIX; 134 156
 FT PT TURN; 157 159
 FT PT HELIX; 161 182
 FT PT TURN; 183 184
 FT SQ SEQUENCE; 187 AA; 22294 MW; OB013D4087723CEC CRC64;
 FT PT HELIX; 24 44
 FT PT HELIX; 63 66
 FT PT HELIX; 73 92
 FT PT TURN; 96 97
 FT PT HELIX; 102 125
 FT PT TURN; 126 128
 FT PT HELIX; 134 156
 FT PT TURN; 157 159
 FT PT HELIX; 161 182
 FT PT TURN; 183 184
 FT SQ SEQUENCE; 187 AA; 22294 MW; OB013D4087723CEC CRC64;
 FT PT HELIX; 24 44
 FT PT HELIX; 63 66
 FT PT HELIX; 73 92
 FT PT TURN; 96 97
 FT PT HELIX; 102 125
 FT PT TURN; 126 128
 FT PT HELIX; 134 156
 FT PT TURN; 157 159
 FT PT HELIX; 161 182
 FT PT TURN; 183 184
 FT SQ SEQUENCE; 187 AA; 22294 MW; OB013D4087723CEC CRC64;
 FT PT HELIX; 24 44
 FT PT HELIX; 63 66
 FT PT HELIX; 73 92
 FT PT TURN; 96 97
 FT PT HELIX; 102 125
 FT PT TURN; 126 128
 FT PT HELIX; 134 156
 FT PT TURN; 157 159
 FT PT HELIX; 161 182
 FT PT TURN; 183 184
 FT SQ SEQUENCE; 187 AA; 22294 MW; OB013D4087723CEC CRC64;
 FT PT HELIX; 24 44
 FT PT HELIX; 63 66
 FT PT HELIX; 73 92
 FT PT TURN; 96 97
 FT PT HELIX; 102 125
 FT PT TURN; 126 128
 FT PT HELIX; 134 156
 FT PT TURN; 157 159
 FT PT HELIX; 161 182
 FT PT TURN; 183 184
 FT SQ SEQUENCE; 187 AA; 22294 MW; OB013D4087723CEC CRC64;
 FT PT HELIX; 24 44
 FT PT HELIX; 63 66
 FT PT HELIX; 73 92
 FT PT TURN; 96 97
 FT PT HELIX; 102 125
 FT PT TURN; 126 128
 FT PT HELIX; 134 156
 FT PT TURN; 157 159
 FT PT HELIX; 161 182
 FT PT TURN; 183 184
 FT SQ SEQUENCE; 187 AA; 22294 MW; OB013D4087723CEC CRC64;
 FT PT HELIX; 24 44
 FT PT HELIX; 63 66
 FT PT HELIX; 73 92
 FT PT TURN; 96 97
 FT PT HELIX; 102 125
 FT PT TURN; 126 128
 FT PT HELIX; 134 156
 FT PT TURN; 157 159
 FT PT HELIX; 161 182
 FT PT TURN; 183 184
 FT SQ SEQUENCE; 187 AA; 22294 MW; OB013D4087723CEC CRC64;
 FT PT HELIX; 24 44
 FT PT HELIX; 63 66
 FT PT HELIX; 73 92
 FT PT TURN; 96 97
 FT PT HELIX; 102 125
 FT PT TURN; 126 128
 FT PT HELIX; 134 156
 FT PT TURN; 157 159
 FT PT HELIX; 161 182
 FT PT TURN; 183 184
 FT SQ SEQUENCE; 187 AA; 22294 MW; OB013D4087723CEC CRC64;
 FT PT HELIX; 24 44
 FT PT HELIX; 63 66
 FT PT HELIX; 73 92
 FT PT TURN; 96 97
 FT PT HELIX; 102 125
 FT PT TURN; 126 128
 FT PT HELIX; 134 156
 FT PT TURN; 157 159
 FT PT HELIX; 161 182
 FT PT TURN; 183 184
 FT SQ SEQUENCE; 18

RESULT 2	22	MSYNLGLFLQRSSNFQCOKLLWQNLGRLEYCLKDRMNFDIPEEIKLQQFQKEDAAALTY 81
Q5YWC9_HUMAN PRELIMINARY; ID Q5YWC9;	61	EMLQNTIAIFRQDSSSTGNETTIVNLLANYHQLNHLKTVEEKEKEDFTRGKLMSSL 120
AC DT 01-FEB-2005 (TREMBrel. 29, Created)	82	EMLQNTIAIFRQDSSSTGNETTIVNLLANYHQLNHLKTVEEKEKEDFTRGKLMSSL 141
DT 01-FEB-2005 (TREMBrel. 29, Last annotation update)	121	HLKRYYGRILHYLAKKEYSHCAWTIVRVEILLRNFFINRLTYLRN 166
DT 13-SEP-2005 (TREMBrel. 31, Last annotation update)	142	HLKRYYGRILHYLAKKEYSHCAWTIVRVEILLRNFFINRLTYLRN 187
DE Interferon, beta 1, fibroblast.		
GN Name=IFNB1; ORFNAMES=RP11-113D19.1-002;		
OS Homo sapiens (Human).		
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homeo;		
OX NCBITaxonID=9606;		
RP [1]		
NUCLEOTIDE SEQUENCE.		
RA Martin S.; Submitted (MAY-2005) to the EMBL/GenBank/DBJ databases.		
RA [2]		
RP NUCLEOTIDE SEQUENCE.		
RC TISSUE=PCR rescued clones; MEDLINE=22388057; PubMed=12477932; DOI=10.1073/pnas.242603899;		
RA Strausberg R.L., Peingold E.A., Grouse L.H., Derge J.G., Schuler G.D., Altshuler S.F., Collins F.S., Wagner C.M., Schaeffer C.F., Bhat N.K., Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F., Diatchenko L., Matsunaga A., Farmer A., Rubin G.M., Hong L., Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E., Brownstein M.J., Tordin T.B., Toshiyuki S., Carninci P., Prange C., Raha S., Loquelle N.A., Peters G.J., Abramson R.D., Mullahy S.J., Bosak S.A., McEwan P.J., Peterson K.J., Malek J.A., Gunaratne P.H., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Villalon D.K., Murzyn D.M., Sodergren E.J., Lu X., Gibbs R.A., Fahay J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A., Whiting M., Madan A., Young A.C., Shevchenko Y., Boutjard G.G., Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalius D.E., Schnarch A., Schein J.E., Jones S.J.M., Marra M.A., "Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences"; Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).		
RA [3]		
RP NUCLEOTIDE SEQUENCE.		
RC TISSUE=PCR rescued clones; NIH MGC Project; Submitted (MAY-2005) to the EMBL/GenBank/DBJ databases.		
CC -1- SUBCELLULAR LOCATION: Secreted (By similarity).		
DR EMBL; AL990882; CAH70160_1; -; Genomic_DNA.		
DR EMBL; BC096151; AAH96151_1; -; mRNA.		
DR EMBL; BC096152; AAH96152_1; -; mRNA.		
DR EMBL; BC096153; AAH96153_1; -; mRNA.		
DR EMBL; BC096150; AAH96150_1; -; mRNA.		
DR Ensemble: ENSG0000171855; Homo sapiens.		
DR GO:GO:0005576; C:extracellular matrix protein binding.		
DR GO:GO:0005126; F:hematopoietin/interferon-class (D200-domain. . .); IEA.		
DR InterPro; IPR000471; Interferon_abd.		
DR Pfam; PF00143; Interferon; 1.		
DR SMART; SM00076; InterferonAB.		
DR PROSITE; PS00252; INTERFERON_A_B_D; 1.		
DR Antiviral defense; Cytokine.		
SQ SEQUENCE: 187 AA; 22294 MW; 0B013D4087723CEC CRC64;		
Query Match Score 874; DB 2; Length 187; Best Local Similarity 100.0%; Score 100.0%; Pred. No. 1.7e-63; Matches 166; Conservative 0; Mismatches 0; Indels 0; Gaps 0;		
Db 22 MSYNLGLFLQRSSNFQCOKLLWQNLGRLEYCLKDRMNFDIPEEIKLQQFQKEDAAALTY 81		
Db 61 EMLQNTIAIFRQDSSSTGNETTIVNLLANYHQLNHLKTVEEKEKEDFTRGKLMSSL 120		
Db 82 EMLQNTIAIFRQDSSSTGNETTIVNLLANYHQLNHLKTVEEKEKEDFTRGKFMVSSL 141		

1 MSYNLGLFLQRSSNFQCOKLLWQNLGRLEYCLKDRMNFDIPEEIKLQQFQKEDAAALTY 60

2 MSYNLGLFLQRSSNFQCOKLLWQNLGRLEYCLKDRMNFDIPEEIKLQQFQKEDAAALTY 81

Qy	121	HLLKRYGRLHLVLAKEYSHCACHTIVRVEILRNFFINRLTGYLRN 166	OC	Sus.
Db	142	HLKRYGRLHLVLAKEYSHCACHTIVRVEILRNFFINRLTGYLRN 187	OX	NCBI_TaxID=9823;
			RN	[1]
			RP	NUCLEOTIDE SEQUENCE.
			RC	TISSUE=Blood;
			RA	Artursson K., Gobl A., Lindersson M., Johansson M., Alm G.;
			RT	"Molecular cloning of a gene encoding porcine interferon-beta.";
			RL	J. Interferon Res. 0:0-0(1992).
			RN	[2]
			RP	NUCLEOTIDE SEQUENCE.
			RX	MEDLINE=92348910; PubMed=1640116;
			RA	Artursson K., Gobl A., Lindersson M., Johansson M., Alm G.;
			RT	"Molecular cloning of a gene encoding porcine interferon-beta.";
			RL	J. Interferon Res. 12:153-160(1992).
			CC	-; SUBCELLULAR LOCATION: Secreted (By similarity).
			DR	EMBL: M86762; AAA31056.1; -; Genomic DNA.
			DR	HSSP: P01574; 1AU.
			DR	GO; GO:0005576; C:extracellular region; IEA.
			DR	GO; GO:0005126; F:hematopoietin/interferon-class (D200-domain. . . ; IEA.
			DR	GO; GO:0006952; P:defense response; IEA.
			DR	InterPro; IPR00471; Interferon_abd.
			PFAM	PF00143; Interferon_1.
			PRINTS	PR00265; INTERFERON_AB.
			PRODOM	PD000550; Interferon_abd; 1.
			SMART	SM00076; IFabd; 1.
			PROSITE	PS0022; INTERFRON_A_B_D; 1.
			KW	Antiviral defense; Cytokine; Signal.
			FT	SIGNAL 1
			FT	21 186 22 186 interferon-beta-1.
			FT	CHAIN 186 AA; 21878 MW; 5F1B8B3C3AE603D CRC64;
			FT	SEQUENCE 186 AA; 21878 MW; 5F1B8B3C3AE603D CRC64;
			Query Match	61.3%; Score 535.5; DB 2; Length 186;
			Best Local Similarity	62.0%; Pred. No. 7.4e-36;
			Matches	103; Conservate 28; Mismatches 34; Indels 1; Gaps 1;
			Qy	1 MSYNLIGFLQSSNFQCQLLWQLNGRLYCLKDQRNFDPPEIKLQQQFKEDALITY 60
			Db	22 MSYDVLRYQRSNTACQKUQGPCTPOYCLEDNMFPEVEEMQPPQFOKEADALITY 81
			Qy	61 EMLQNIAIFAFQDSSSTGNNETTANLYHQINHLKVLEEKEDFTRGKLMSSL 120
			Db	82 EMLQQFGIILRRNFSSTGNNETVKITLVELGDQMDLTLEEIMEEENPFRGD-MTIL 140
			Qy	121 HLKRYGRLHLVLAKEYSHCACHTIVRVEILRNFFINRLTGYLRN 166
			Db	141 HLKKYTLISIOLYLSKEYRSCAWTVQVETLRNFSFLNRDYLRN 186
			RESULT	6
			ID	Q681Q4_PIG PRELIMINARY;
			AC	Q681Q4_AA.
			DT	25-Oct-2004 (TrEMBLrel. 28; Created)
			DT	25-Oct-2004 (TrEMBLrel. 28; Last sequence update)
			DT	25-Oct-2004 (TrEMBLrel. 28; Last annotation update)
			DE	Interferon beta protein.
			OS	Sus scrofa (Pig).
			OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Cetartiodactyla; Suisina; Suidae; Sus.
			OC	OC Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Suina; Suidae;
			OX	NCBI_TaxID=9823;
			RN	[1]
			RP	NUCLEOTIDE SEQUENCE.
			RA	Qian P., Peng G.Q., Li X.M., Yao Q.X., Xu Z.F., Guo D.C., Chen H.C.;
			RT	"Clone and analysis of meishan porcine interferon beta gene.";
			RL	Submitted (JUL-2004) to the EMBL/GenBank/DBJ databases.
			CC	-; SUBCELLULAR LOCATION: Secreted (By similarity).
			DR	EMBL: AY687281; AATP8375.1; - mRNA.
			DR	GO; GO:0005576; C:extracellular region; IEA.
			DR	GO; GO:0005126; F:hematopoietin/interferon-class (D200-domain. . . ; IEA.
			DR	GO; GO:0006952; P:defense response; IEA.
			DR	InterPro; IPR00471; Interferon_abd.

DR	PFam; PF00143; Interferon; 1.						
DR	PRINTS; PR00266; INTERFERON_AB.						
DR	PRODOM; PD00050; Interferon_abd; 1.						
DR	SMART; SM00076; Iraabd; 1.						
DR	PROSITE; PS00252; INTERFERON_A_B_D; 1.						
KW	Antiviral defense; Cytokine; Sequence 186 AA;						
SQ	MSNLGFLQSRSSNFOCQLLWLQNGRLLEYCLKDRAFNDFPERIKOLQFOKEADAALTY 60 SEQUENCE 186 AA; 21950 MW; 79D70553C3ADD6DC CRC64;						
Query Match	61.2%; Score 534.5; DB 2; Length 186;						
Best Local Similarity	62.0%; Pred. No. 8.0e-36;						
Matches	103; Conservative 28; Mismatches 34; Indels 1; Gaps 1;						
Qy	1 MSNLGFLQSRSSNFOCQLLWLQNGRLLEYCLKDRAFNDFPERIKOLQFOKEADAALTY 60	59.8%; Score 522.5; DB 1; Length 186;					
Db	22 VSYKLQFQLRSSLSCEQELLYLNNTSKYCLKDRAFNFEVPEEIKSQRFOKEAALVIN 81	61.1%; Pred. No. 8.5e-35; Indels 1; Gaps 1;					
Query Match	61.2%; Score 534.5; DB 2; Length 186;						
Best Local Similarity	62.0%; Pred. No. 8.0e-36;						
Matches	103; Conservative 28; Mismatches 34; Indels 1; Gaps 1;						
Qy	1 MSNLGFLQSRSSNFOCQLLWLQNGRLLEYCLKDRAFNDFPERIKOLQFOKEADAALTY 60	59.8%; Score 522.5; DB 1; Length 186;					
Db	22 MSTDVLVRQSRSSNLACQKLLQPLGTPQYCYLEDRAFNDFPERIKOLQFOKEADAALTY 81	61.1%; Pred. No. 8.5e-35; Indels 1; Gaps 1;					
Query Match	61.2%; Score 534.5; DB 2; Length 186;						
Best Local Similarity	62.0%; Pred. No. 8.0e-36;						
Matches	103; Conservative 28; Mismatches 34; Indels 1; Gaps 1;						
Qy	1 MSNLGFLQSRSSNFOCQLLWLQNGRLLEYCLKDRAFNDFPERIKOLQFOKEADAALTY 60	59.8%; Score 522.5; DB 1; Length 186;					
Db	22 MSTDVLVRQSRSSNLACQKLLQPLGTPQYCYLEDRAFNDFPERIKOLQFOKEADAALTY 81	61.1%; Pred. No. 8.5e-35; Indels 1; Gaps 1;					
Query Match	61.2%; Score 534.5; DB 2; Length 186;						
Best Local Similarity	62.0%; Pred. No. 8.0e-36;						
Matches	103; Conservative 28; Mismatches 34; Indels 1; Gaps 1;						
Qy	1 MSNLGFLQSRSSNFOCQLLWLQNGRLLEYCLKDRAFNDFPERIKOLQFOKEADAALTY 60	59.8%; Score 522.5; DB 1; Length 186;					
Db	22 MSTDVLVRQSRSSNLACQKLLQPLGTPQYCYLEDRAFNDFPERIKOLQFOKEADAALTY 81	61.1%; Pred. No. 8.5e-35; Indels 1; Gaps 1;					
RESULT 7							
IFNB_FELCA	ID IFNB_FELCA STANDARD; PRT; 186 AA.						
AC	QnN7J0; 16-OCT-2001 (Rel. 40, Created)						
DT	16-OCT-2001 (Rel. 40, Last sequence update)						
DT	10-MAY-2005 (Rel. 47, Last annotation update)						
DT	Interferon beta precursor (IFN-beta).						
DN	Name=IFNB1; Synonyms=IFNB;						
OS	Felis silvestris catus (Cat); Chordata; Craniata; Vertebrata; Euteleostomi;						
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;						
OC	Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Felidae;						
RN	NCBI_TaxID=9685; RN						
RP	NUCLEOTIDE SEQUENCE.						
RA	Murakami Y., Kubota T., Mochizuki M., Kishi M.; "Genetic structure of feline interferon beta."						
RT	"Submitted (DEC-1998) to the EMBL/GenBank/DBJ databases.						
CC	-!- FUNCTION: Has antiviral, antibacterial and anticancer activities (By similarity).						
CC	-!- SUBCELLULAR LOCATION: Secreted.						
CC	-!- SIMILARITY: Belongs to the alpha/beta interferon family.						
CC	NUCLEOTIDE SEQUENCE.						
RA	Murakami Y., Kubota T., Mochizuki M., Kishi M.; "Genetic structure of feline interferon beta."						
RT	"Submitted (DEC-1998) to the EMBL/GenBank/DBJ databases.						
CC	-!- FUNCTION: Has antiviral, antibacterial and anticancer activities (By similarity).						
CC	-!- SUBCELLULAR LOCATION: Secreted.						
CC	-!- SIMILARITY: Belongs to the alpha/beta interferon family.						
CC	This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not removed.						
CC						
DR	EMBL; AB21707; BA93629; 1; ; Genomic DNA.						
DR	HSSP; P01574; 1AU1.						
DR	InterPro; IPR000471; Interferon_abd.						
DR	PANTHER; PT0011691; Interferon_abd; 1.						
DR	PFam; PF00143; Interferon; 1.						
DR	PRODOM; PD000550; INTERFERONAB.						
DR	PROSITE; PS00252; INTERFERON_AB_D; 1.						
KW	Antiviral defense; Cytokine; Glycoprotein; Signal.						
PY	SIGNAL_1						
PT	CHAIN 22 186 Interferon beta.						
PT	CARBHYD 46 46 N-linked (GlcNAc. .) (Potential).						
PT	CARBHYD 101 101 N-linked (GlcNAc. .) (Potential).						
PT	CARBHYD 131 131 N-linked (GlcNAc. .) (Potential).						
PT	CARBHYD 136 136 N-linked (GlcNAc. .) (Potential).						
PT	CARBHYD 52 161 By similarity.						
SQ	SEQUENCE 186 AA; 22188 MW; 25C359B1808AC862 CRC64;						
Query Match	59.8%; Score 522.5; DB 1; Length 186;						
Best Local Similarity	61.1%; Pred. No. 8.5e-35; Indels 1; Gaps 1;						
Matches	102; Conservative 27; Mismatches 36; Indels 1; Gaps 1;						
Qy	1 MSNLGFLQSRSSNFOCQLLWLQNGRLLEYCLKDRAFNDFPERIKOLQFOKEADAALTY 60	59.8%; Score 522.5; DB 1; Length 186;					
Db	22 VSYKLQFQLRSSLSCEQELLYLNNTSKYCLKDRAFNFEVPEEIKSQRFOKEAALVIN 81	61.1%; Pred. No. 8.5e-35; Indels 1; Gaps 1;					
Query Match	61.2%; Score 534.5; DB 2; Length 186;						
Best Local Similarity	62.0%; Pred. No. 8.0e-36;						
Matches	103; Conservative 28; Mismatches 34; Indels 1; Gaps 1;						
Qy	1 MSNLGFLQSRSSNFOCQLLWLQNGRLLEYCLKDRAFNDFPERIKOLQFOKEADAALTY 60	59.8%; Score 522.5; DB 1; Length 186;					
Db	22 MSTDVLVRQSRSSNLACQKLLQPLGTPQYCYLEDRAFNDFPERIKOLQFOKEADAALTY 81	61.1%; Pred. No. 8.5e-35; Indels 1; Gaps 1;					
RESULT 8							
IFNB2_BOVIN	ID IFNB2_BOVIN STANDARD; PRT; 186 AA.						
AC	P01576; 21-JUL-1986 (Rel. 01, Created)						
DT	21-JUL-1986 (Rel. 01, Last sequence update)						
DT	10-MAY-2005 (Rel. 47, Last annotation update)						
DB	Interferon beta-2 precursor.						
GN	Name=IFNB2;						
OS	Bos taurus (Bovine).						
OC	Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;						
OC	Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;						
OC	pecora; Bovidae; Bovinae; Bos.						
NCBI_TaxID	9913; [1];						
RN							
RP	NUCLEOTIDE SEQUENCE.						
RA	Leung D.W., Capon D.J., Goeddel D.V.; "The structure and bacterial expression of three distinct bovine interferon-beta genes"; Biotechnology (N.Y.) 2:458-464(1994).						
RT	This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not removed.						
CC	-!- SIMILARITY: Belongs to the alpha/beta interferon family.						
CC	-!- SUBCELLULAR LOCATION: Belongs to the alpha/beta interferon family.						
DR	EMBL; M15478; AAA30580; 1; ; Genomic_DNA.						
DR	PfR; A01840; IVB052.						
DR	HSSP; P01574; 1AU1.						
DR	InterPro; IPR00471; Interferon_abd.						
DR	PANTHER; PT0011691; Interferon_abd; 1.						
DR	PFam; PF00143; Interferon; 1.						
DR	PRODOM; PD000550; INTERFERONAB.						
DR	PROSITE; PS00252; INTERFERON_AB_D; 1.						
KW	Antiviral defense; Cytokine; Glycoprotein; Signal.						
PT	SIGNAL_1						
PT	CHAIN 21 186 Interferon beta.						
FT	N_Linked (GlcNAc. .) (Potential).						
FT	CHAIN 22 186 N_Linked (GlcNAc. .) (Potential).						
FT	CARBHYD 131 131 N_Linked (GlcNAc. .) (Potential).						
FT	CARBHYD 173 173 N_Linked (GlcNAc. .) (Potential).						
FT	DISULFID 52 161 Probable.						
SQ	SEQUENCE 186 AA; 2319 MW; D9F25/C6E3250480 CRC64;						
Query Match	56.4%; Score 492.5; DB 1; Length 186;						
Best Local Similarity	57.9%; Pred. No. 2.4e-32; Indels 30; Mismatches 38; Indels 1; Gaps 1;						
Matches	95; Conservative 30; Mismatches 38; Indels 1; Gaps 1;						
Qy	2 SYNLLGFLQSRSSNFOCQLLWLQNGRLLEYCLKDRAFNDFPERIKOLQFOKEADAALTY 61	59.8%; Score 522.5; DB 1; Length 186;					
Db	SYSLRFQRRSLALCQKLRLQPSTPQHLCMDFQMPPEENKQQAQOFQKEADLVYE 82	61.1%; Pred. No. 8.5e-35; Indels 1; Gaps 1;					

Qy 62 MLQNIAIFRQSSSTGNNETIVENILANYHQINHLKTVLEEKEDFTRGKLMSSLH 121
 Db 83 MIQQQIFNLTREDSTSETTIDLLEELYEQMNNHLEPIQEIMOKQNSTMGD-TTVLH 141

Qy 122 LKRYYGRILHYLKAKEYSHCAWTIVRLNFYFIRNLTYGLR 165
 Db 142 LRKYFYENLVQYLKSKEYNRCAWTVRVQLRNFSFLTRGGLR 185

RESULT 9
 IFNB₁ HORSE STANDARD PRT; 186 AA.
 AC P05012;
 DT 13-AUG-1987 (Rel. 05, Created)
 DT 13-AUG-1987 (Rel. 05, Last sequence update)
 DE Interferon beta precursor (IFN-beta).
 GN Name=IFNB1; Synonyms=IFNB;
 OC Equus caballus (Horse).
 Mammalia; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Laurasiatheria; Perissodactyla; Equidae; Equus.
 NCBI_TaxID=9796;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 MEDLINE=8703170; PubMed=2022999;
 RA Himmelman R., Hauptmann R., Adolf G.R., Swtely P.;
 RT "Molecular cloning and expression in Escherichia coli of equine type I
 interferons".
 RL DNA 5:345-356 (1986).
 CC -1- FUNCTION: Has antiviral, antibacterial and anticancer activities.
 CC -1- SUBUNIT: Monomer.
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- SIMILARITY: Belongs to the alpha/beta interferon family.

This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation at the European Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not removed.

CC DR EMBL; M14546; AA30954.1; -; Genomic_DNA.
 CC DR PIR; A01841; IUBOB3.
 CC DR HSSP; P01574; IAU1.
 CC DR InterPro; IPR00471; Interferon_abd.
 CC DR PANTHER; PTHR11691; Interferon_abd; 1.
 CC DR Pfam; PF00143; Interferon; 1.
 CC DR PRINTS; PR00266; INTERFRON_AB.
 CC DR ProDom; PD000550; Interferon abd; 1.
 CC DR PROSITE; PS00232; INTERFRON_A_B_D; 1.
 CC DR KW Antiviral defense; Cytokine; Glycoprotein; Multigene family; Signal.
 CC DR SIGNAL 1
 CC DR CHAIN 22 186 Interferon beta-3.
 CC DR FT CARBOHYD 131 131 N-linked (GlcNAc. .) (Potential).
 CC DR FT CARBOHYD 173 173 N-linked (GlcNAc. .) (Potential).
 CC DR FT DISUFRID 52 161 Probable.
 CC DR SQ SEQUENCE 186 AA; 22060 MW; 1D10111EBEE1A65D CRC64;

Query Match 52.5% Score 458.5; DB 1; Length 186;
 Best Local Similarity 53.3%; Pred. No. 1.4e-29; Indels 1; Gaps 1;
 Matches 88; Conservative 35; Mismatches 41;

Qy 2 SYNLLGFLQRSSNNFOCQKLWLNGLREYCLKDRMNFDIPEIKQLQQFQKEADAALTYE 61
 Db 83 MLQQINILITRDFTSSGWSSETTIDLIVELYQMRNQPIOKEIQNFQVPEEMNQAOQFREDAVIVYE 82

Qy 62 MLQNIAIFRQSSSTGNNETIVENILANYHQINHLKTVLEEKEDFTRGKLMSSLH 121
 Db 83 MLQQINILITRDFTSSGWSSETTIDLIVELYQMRNQPIOKEIQNFQVPEEMNQAOQFREDAVIVYE 82

RESULT 11
 IFNB₁ BOVIN STANDARD PRT; 186 AA.
 AC P01578;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)

Qy 1 MSYNLIGFLQRSSNNFOCQKLWLNGLREYCLKDRMNFDIPEIKQLQQFQKEADAALTYE 60
 Db 22 VNDDLRSQQLRSNSACMMLRQNGAQRCPDDTNFQVPEBIEQAOQFQKEADAALTYV 81

Qy 61 EMQNIAIFRQSSSTGNNETIVENILANYHQINHLKTVLEEKEDFTRGKLMSSL 120
 Db 82 EMQHQTWRERRFASTSWNETVKNLVYQMLDRTEUNEEBEESSTWGN-TTIL 140

Qy 121 HKRYYGRILHYLKAKEYSHCAWTIVRLNFYFIRNLTYGLR 166
 Db 141 RLKYYGRISQYKAKRYSHCAWTQVQAEMLRNLAFLNGLDYLN 186

-!- FUNCTION: Has antiviral, antibacterial and anticancer activities.
 CC -!- SUBUNIT: Monomer (By similarity).
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- PTM: This beta interferon does not have a disulfide bond.
 CC -!- SIMILARITY: Belongs to the alpha/beta interferon family.

This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation at the European Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not removed.

CC DR EMBL; D87919; BAA13502.1; -; Genomic_DNA.
 CC DR PIR; JC5424; JC5424.
 CC DR HSSP; P01574; 1AU1.
 CC DR SMR; P70493; 22-184.
 CC DR Ensembl; ENSEMBL000000006268; Rattus norvegicus.
 CC DR RGD; 2865; Ifambi.
 CC DR Interpro; IPR00471; Interferon_abd.
 CC DR PANTHER; PTHR11691; Interferon_abd; 1.
 CC DR Pfam; PF00143; Interferon; 1.
 CC DR PRINTS; PRO0266; INTERFERONAB.
 CC DR ProdDom; PD000550; Interferon_abd; 1.
 CC DR PROSITE; PS00255; INTERFERON_AB_D; 1.
 CC KW Antiviral defense; Cytokine; Glycoprotein; Signal.
 CC FT SIGNAL_1 21 By similarity.
 CC FT CHAIN_1 184 Interferon beta.
 CC FT CARBOHYD_50 50 N-linked (GlcNAc. . .) (Potential).
 CC FT CARBOHYD_92 92 N-linked (GlcNAc. . .) (Potential).
 CC FT CARBOHYD_99 99 N-linked (GlcNAc. . .) (Potential).
 CC FT CARBOHYD_171 171 N-linked (GlcNAc. . .) (Potential).
 CC SQ SEQUENCE 184 AA; 22073 MW; 1D051D23F979ADDE CRC64; 184

Query Match 38.4%; Score 335.5; DB 1; Length 184;
 Best Local Similarity 45.8%; Pred. No. 1.5e-19;
 Matches 76; Conservative 24; Mismatches 63; Indels 3; Gaps 2;

Qy	1 MSNLIGFLQRSSNFQOCQKLIWOLNGLREYCLDKRMNFDPPEEITKOLQQFOKEDDAIALI 60
Db	22 IDYKQQLQFQSSTSRICQKLLRQLNRLN - LSYTRDFKLPMEVNHPSQMKSYTAFQI 79
Qy	61 EMLQNLPAIQPQDSSTGNNETIVENILANVYHQINHLKTVLBEELKEFDTRGKLMSSL 120
Db	80 VMLQNLVFLVRSNFNSSTGNNETIVESLSDLHQQTELEITLKEK-QEERLTWVTSSTTTL 138
Qy	121 HLRKRYGRILHLYKAKEYSHCAWTIVRVELLRFNFIRNLTYLERN 166
Db	139 GLKSYTWRVQRYLKDQKRNSTAWMYRAEVFRNFSTILRBNRFQN 184

Name=IFN;
 OS Macropus eugenii (Tammar wallaby).
 OC Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Metatheria; Diprotodontia; MacroPodidae; Macropus.
 OC NCB_I_TaxID:9315;

RESULT 14
 Q7YRX6 MACEU PRELIMINARY;
 ID Q7YRX6_1 MACEU PRELIMINARY;
 AC Q7YRX6;
 DT 01-OCT-2003 (TREMBLrel. 25, Created)
 DT 01-OCT-2003 (TREMBLrel. 25, Last sequence update)
 DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)
 DE Interferon beta 1.
 GN Name=IFN;
 OS Macropus eugenii (Tammar wallaby).
 OC Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Metatheria; Diprotodontia; MacroPodidae; Macropus.
 OC NCB_I_TaxID:9315;

RP NUCLEOTIDE SEQUENCE.
 RX PubMed:1518033; DOI:10.1016/j.dci.2004.02.002;
 RA Harrison G.A.; McNicol K.A.; Deane E.M.;
 RT "Interferon alpha/beta genes from a marsupial, *Macropus eugenii*";
 RL Dev. Comp. Immunol. 28:927-940 (2004).
 CC -!- SUBCELLULAR LOCATION: Secreted (By similarity).
 DR EMBL; AY165862; AA037658.1; -; Genomic_DNA.
 DR HSSP; P01574; 1AU1.
 DR GO; P005576; C:extracellular region; IEA.

Qy 121 HLKRYGRILHHLKAKEYSHCAWTIVRVEELLRNFEVFINRTGYL R 165
 | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | :
Db 142 HIKSYFKRMMDLKGKNYSSCAWEVIRMETRSCLVYRLTRKLK 186

Search completed: December 21, 2005, 14:21:43
Job time : 229 secs

RESULT 15						
	Q6XZM6	9MAMM	PRT;	187 AA.		
ID	Q6XZM6_9MAMM	PRELIMINARY;				
AC	Q6XZM6_					
DT	05-JUL-2004	(TREMBLrel. 27, Created)				
DT	05-JUL-2004	(TREMBLrel. 27, Last sequence update)				
DT	05-JUL-2004	(TREMBLrel. 27, Last annotation update)				
DE	Interferon-beta.					
OS	Tachyglossus aculeatus (Australian echidna).					
OC	Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Monotremata; Tachyglossidae; Tachyglossus.					
OX	NCBI_TaxID:9261;					
RN	[1]					
RP	NUCLEOTIDE SEQUENCE.					
	PubMed:15661761; DOI: 10.1046/j.0818-9641.2004.01230.x;					
RA	Harrison G.A.; McNicoll K.A.; Deane B.M.;					
RT	"Type I interferon genes from the egg-laying mammal, <i>Tachyglossus aculeatus</i> (short-beaked echidna)";					
RL	Immunol. Cell Biol. 82:112-118(2004).					
CC	-! - SUBCELLULAR LOCATION: Secreted (By similarity).					
DR	EMLAY; AY194920; AAP34279.1; - Genomic_DNA.					
DR	HSSP; P01574; IAU1.					
GO	GO:000576; C: extracellular region; IEA.					
GO	GO:0005126; F: hematopoietin/interferon-class (D200-domain. . . ; IEA.					
DR	GO:0006952; P: defense response; IEA.					
DR	InterPro; IPR00471; Interferon_abd.					
PFam	PF00143: Interferon_1.					
DR	PRINTS; PRO0266; INTERFERONAB.					
DR	ProDom; SM00076; Interferon_abd; 1.					
DR	SMART; SM00076; IFand; 1.					
DR	PROSITE; PS00250; INTERFERON_A_B_D; UNKNOWN_1.					
KW	Antiviral defense; Cytokine.					
SEQUENCE	187 AA; 22496 MW; 00A7FAC603EA50E5 CRC64;					
Query Match Score	3.44 %;	Score 301;	DB 2;	Length 187;		
Best Local Similarity 40.6 %;	Pred. No. 1e-16;	Mismatches 59;	Indels 2;	Gaps .		
Matches 67; Conservative 37;						
Qy 2 SYNLGFQLRSNSNFOCQKLLWQNGLRL-EYLKDRMNFDIPEEEIKLOOQFOKEADALTIY 60						
Db 23 SYLELYSHQWLNWNKWSLHLNLSLDGQFPLHCKRESNMFKLPAEMLPHQFOQEENATEAH 82						
Qy 61 EMLQNIQIAIPQDQSSTGWNTIVENILANVYHQINHLKTVLEKLEKDFTRGKLMSSL 124						
Db 83 DQIQCQENIFVPSIISGNSHTGWDAAVEKLHGTHQEMWVLEELFEEWNGWTSLLRJDJ-SL 14						

THIS PAGE BLANK (USPTO)

Gencore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using BW model

Run on: December 21, 2005, 13:55:56 ; Search time 187 Seconds
 390.037 Million cell updates/sec

Title: US-10-084-706-2

Perfect score: 874

Scoring table: BLOSUM62

Sequence: 1 MSYNIILGFLQRSSNFQCQKL.....RVEILRNFYFIRNLTGYLRN 166

Gapext: 0.5

Searched: 2443163 seqs, 4393781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Maximum Match 0*

Listing first 45 summaries

Database : A_Geneseq_21;*

1: geneseqP19808;*

2: geneseqP19905;*

3: geneseqP20008;*

4: geneseqP20018;*

5: geneseqP20028;*

6: geneseqP20038;*

7: geneseqP20048;*

8: geneseqP20048;*

9: geneseqP20058;*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,

and is derived by analysis of the total score distribution.

ALIGNMENTS

RESULT 1

AAP30219
ID AAP30219 standard; protein; 166 AA.

XX
AC AAP30219;

DT 25-MAR-2003 (revised)

DT 25-MAY-1992 (first entry)

XX
Sequence of interferon (HuIFN) -beta-1 encoded by plasmid pDM101/trp/beta-1.

XX
Hybrid interferon; antiviral; therapy; cancer; tumour.
XX
Homo sapiens.

OS XX

PN WOB302461-A.

DE -1.

DE 44

DE 45

DE 874

DE 100.0

DE 166

DE 8

DE 166

DE 7

DE 166

the 74-1167 seq. of HuIFN-alpha-1 resp.). (see AAN30156, AAP30223). In the examples plasmids pgM5 and pDM101/trp/beta-1 and p-alpha-61A were used (see AAN30151, AAN30152, AAN30157). RinfI was used to digest the DNA sequences in the region of significant handicaps (see AAN30153, AAN30154, AAN30158, AAN30159), and the restriction fragments were ligated to form hybrid DNA. (updated on 25-MAR-2003 to correct PA field.)

Sequence 166 AA;

Query Match 100.0%; Score 874; DB 1; Length 166;
Best Local Similarity 100.0%; Pred. No. 2.1e-69;
Matches 166; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

SQ 1 MSYNLIGFLQRSSNFQOKLWQNLNGRLEYCLKDMMNFIDPEEIKQLQQFQKEDALITY 60
Db 1 MSYNLIGFLQRSSNFQOKLWQNLNGRLEYCLKDMMNFIDPEEIKQLQQFQKEDALITY 60

Qy 1 MSYNLIGFLQRSSNFQOKLWQNLNGRLEYCLKDMMNFIDPEEIKQLQQFQKEDALITY 60
Db 1 MSYNLIGFLQRSSNFQOKLWQNLNGRLEYCLKDMMNFIDPEEIKQLQQFQKEDALITY 60

Qy 1 EMLQNIAFAIPFQDSSSTGWNNTIVENILANYHQINHLKTIVLEEKEDFTRGKLMSSL 120
Db 1 EMLQNIAFAIPFQDSSSTGWNNTIVENILANYHQINHLKTIVLEEKEDFTRGKLMSSL 120

Qy 1 HLRKYGRILHYLKAKEYSHCAWTIVRLRNFTYFINRLTGYLN 166
Db 1 HLRKYGRILHYLKAKEYSHCAWTIVRLRNFTYFINRLTGYLN 166

Qy 61 EMLQNIAFAIPFQDSSSTGWNNTIVENILANYHQINHLKTIVLEEKEDFTRGKLMSSL 120
Db 61 EMLQNIAFAIPFQDSSSTGWNNTIVENILANYHQINHLKTIVLEEKEDFTRGKLMSSL 120

RESULT 3
AAP50279
ID AAP50279 standard; protein; 166 AA.
XX
AC AAP50279;
XX DT 25-MAR-2003 (revised)
DT 09-DEC-1991 (first entry)
XX DE Protein sequence encoding synthetic interferon-beta gene.
XX KW Interferon-beta; antitumor; immunostimulant.
XX OS Synthetic.
XX PN EP131816-A.
XX PD 23-JAN-1985.
XX PF 28-JUN-1984; 84EP-00107498.
XX PR 01-JUL-1983;
XX PA (SEAR) SEARLE & CO G D.
XX WPI: 1985-020165/04.
DR N-PSDB; AAN50306.

XX PT New modified beta-interferon(s) - useful as antiviral, anti-neoplastic and immuno-modulatory agents.
XX PS Disclosure: Fig 20; 96pp; English.

XX CC The sequence encodes a synthetic interferon-beta which has increased biological activity compared to natural IFN-beta, and which is more effective in the treatment of viral or neoplastic diseases or immunosuppressed or immunodeficient conditions. (Updated on 25-MAR-2003 to correct PA field.)

SQ Sequence 166 AA;

Query Match 100.0%; Score 874; DB 1; Length 166;
Best Local Similarity 100.0%; Pred. No. 2.1e-69;
Matches 166; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MSYNLIGFLQRSSNFQOKLWQNLNGRLEYCLKDMMNFIDPEEIKQLQQFQKEDALITY 60
Db 1 MSYNLIGFLQRSSNFQOKLWQNLNGRLEYCLKDMMNFIDPEEIKQLQQFQKEDALITY 60

Qy 61 EMLQNIAFAIPFQDSSSTGWNNTIVENILANYHQINHLKTIVLEEKEDFTRGKLMSSL 120
Db 61 EMLQNIAFAIPFQDSSSTGWNNTIVENILANYHQINHLKTIVLEEKEDFTRGKLMSSL 120

Qy 121 HLRKYGRILHYLKAKEYSHCAWTIVRLRNFTYFINRLTGYLN 166

Db	121 HLKRYGRLHYLAKAEYSHCAWTIVRVEILRNFYFINRLTGILRN 166 HLKRYGRLHYLAKAEYSHCAWTIVRVEILRNFYFINRLTGILRN 166	Qy	121 HLKRYGRLHYLAKAEYSHCAWTIVRVEILRNFYFINRLTGILRN 166 HLKRYGRLHYLAKAEYSHCAWTIVRVEILRNFYFINRLTGILRN 166
RESULT 4			
Db	AAP61071 standard; protein; 166 AA.	Qy	121 HLKRYGRLHYLAKAEYSHCAWTIVRVEILRNFYFINRLTGILRN 166 HLKRYGRLHYLAKAEYSHCAWTIVRVEILRNFYFINRLTGILRN 166
XX	AC AAP61071;	Db	121 HLKRYGRLHYLAKAEYSHCAWTIVRVEILRNFYFINRLTGILRN 166
XX	DT 03-OCT-2002 (revised)	RESULT 5	
XX	DT 28-MAY-1991 (first entry)	ID AAP70296 standard; protein; 166 AA.	
XX	DE Oxidation resistant mutein of Interferon-Beta.	XX	
XX	DE Sequence of interferon-beta.	XX	
XX	KW Antiviral; antiproliferative agent.	XX	
XX	OS Homo sapiens.	OS Homo sapiens.	
XX	Key Location/Qualifiers	XX	
FT Misc-difference 1_6	/note= "May be N-terminal truncated or absent"	XX	
FT Misc-difference 17	/note= "May be any conservative AA"	XX	
FT Misc-difference 36	/note= "May be any conservative AA"	XX	
FT Misc-difference 62	/note= "May be any conservative AA"	XX	
FT Misc-difference 62	/note= "May be any conservative AA"	XX	
FT Misc-difference 117	/note= "May be any conservative AA"	XX	
XX	AU8652451-A.	XX	
PN	PD 1987-258309/37.	XX	
XX	Conjugates of interferon(s)-beta and gamma - useful as antivirals and anti-cell proliferatives with broader spectrum of activity and obcd.	XX	
XX	PT The inventors claim an interferon conjugate wherein a C-terminal of the region exhibiting biological activities of interferon-beta has been linked to an N-terminal of the region exhibiting biological activities of interferon gamma. The antiviral activity of the conjugate was tested using FL cells-sindbis virus system according to the CPE 50 inhibition method. Antiviral activity ranged from 200 U/ml to 18500 U/ml	XX	
XX	PS Claim 7; p35; 52pp; English.	XX	
XX	CC The inventors claim an interferon conjugate wherein a C-terminal of the region exhibiting biological activities of interferon-beta has been linked to an N-terminal of the region exhibiting biological activities of interferon gamma. The antiviral activity of the conjugate was tested using FL cells-sindbis virus system according to the CPE 50 inhibition method. Antiviral activity ranged from 200 U/ml to 18500 U/ml	XX	
XX	SQ Sequence 166 AA;	XX	
XX	Query Match Score 874; DB 1; Length 166;	XX	
XX	Best Local Similarity 100.0%; Pred. No. 2.1e-60;	XX	
XX	Matches 166; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	XX	
PS	Claim 5; Page 50; 50pp; English.	Qy	1 M\$TNLGFQRSSNFCQQKLWQNGLREYCLKDMMFDIPEEKQLOQFOKEADALITY 60
XX	CC Modified peptide has residues susceptible to chloramine T and peroxide oxidation replaced with conservative AAs. Mutein is thus resistant to oxidation. Other proteins which may be similarly rendered resistant to include tissue plasminogen activator, colony stimulating factor and human growth factor. (Updated on 03-OCT-2002 to add missing OS field.)	Db	1 M\$TNLGFQRSSNFCQQKLWQNGLREYCLKDMMFDIPEEKQLOQFOKEADALITY 60
XX	CC Sequence 166 AA;	Qy	61 EMLQNIFAIFPQDSSSTGWNETIVNLANYHQINHLTVLEEKLEDFTRKLMSSL 120
XX	PS Query Match Score 874; DB 1; Length 166;	Db	61 EMLQNIFAIFPQDSSSTGWNETIVNLANYHQINHLTVLEEKLEDFTRKLMSSL 120
XX	Best Local Similarity 100.0%; Pred. No. 2.1e-69;	Qy	121 HLKRYGRLHYLAKAEYSHCAWTIVRVEILRNFYFINRLTGILRN 166
XX	Mismatches 166; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	Db	121 HLKRYGRLHYLAKAEYSHCAWTIVRVEILRNFYFINRLTGILRN 166
Qy	1 M\$YNLGFQRSSNFCQQKLWQNGLREYCLKDMMFDIPEEKQLOQFOKEADALITY 60	RESULT 6	
Db	1 M\$YNLGFQRSSNFCQQKLWQNGLREYCLKDMMFDIPEEKQLOQFOKEADALITY 60	ID AAP81774	
Qy	61 EMLQNIFAIFPQDSSSTGWNETIVNLANYHQINHLTVLEEKLEDFTRKLMSSL 120	ID AAP81774;	
Db	61 EMLQNIFAIFPQDSSSTGWNETIVNLANYHQINHLTVLEEKLEDFTRKLMSSL 120	XX	
		DT 29-JAN-1999 (first entry)	

XX	Human native interferon-beta protein.	PD	23-MAY-2000.
DE		XX	
XX	Interferon-Beta; variant; human; medicament; treatment; screening;	PF	16-DEC-1997;
KW	multiple sclerosis; measurement; water soluble.	XX	97BR-00010827.
XX		PR	16-DEC-1997;
KW		XX	97BR-00010827.
XX		PA	(UIMI-) UNIV FEDERAL MINAS GERAIS.
OS		XX	
Homo sapiens.		Pereirino Ferreira PC, Rolland Coligher R, Geessien Kroon E;	
XX	DE19717864 A1.	PI	Bonjardim CA, Fiorini De Carvalho A, Rodrigues Dos Santos J;
XX	PN	XX	
XX	PD 29-OCT-1998.	DR	
XX	XX	XX	
PF	23-APR-1997; 97DE-01017864.	PT	Production of recombinant human amniotic membrane interferon comprises
XX	XX	PT	cell cultivation for infection with Sendai virus, production of mRNA, RNA
PR	23-APR-1997; 97DE-01017864.	PT	fractionation, dissolution.
XX		PT	
PA	(FRAU) FRAUNHOFER GES FOERDERUNG ANGEWANDTEN.	PS	Disclosure; Fig 1; 16pp; Portuguese.
XX		PS	
PI	Schneider-Fresenius C, Otto B, Waschuetz G;	XX	
XX	WPI; 1998-569784/4.	CC	This invention relates to a novel method for producing human amniotic
DR		CC	membrane beta-interferon (IFN) protein (also identified as beta-IFN type
XX		CC	1). Specifically, it refers to production of the recombinant protein
PT	New mutated recombinant human interferon-beta protein contains hydroxylic	CC	through genetic engineering techniques that can be used in medicine,
PT	amino acid substitutions to improve water solubility - used e.g. in in	CC	veterinary science and research. In particular, the human amniotic
PT	vitro screening assays, to measure interferon levels and to treat	CC	membrane beta-IFN protein is important in the regulation of growth and
PT	multiple sclerosis.	CC	cellular differentiation and the immunoregulation of biological systems.
XX		CC	The present invention describes the process of cDNA amplification,
PS	Disclosure; Fig 1; 18pp; German.	CC	cloning and transforming competent bacteria then selecting those clones
XX		CC	that express the beta-IFN protein, which is then extracted and purified.
XX		CC	This polypeptide sequence is the human beta-IFN protein of the invention.
XX	Sequence 166 AA;	CC	
SQ		Query Match	100.0%; Score 874; DB 3;
		Best Local Similarity	100.0%; Pred. No. 2.1e-69;
		Matches	0; Mismatches 0; Indels 0; Gaps 0;
Qy	1 MSYNLIGFLQRSSNFOCQLLWQNLGRLEYCLKDRLNFIDPEIKQLQQFKEDDAALTY 60	Db	1 MSYNLIGFLQRSSNFOCQLLWQNLGRLEYCLKDRLNFIDPEEKQLQQFKEDDAALTY 60
Db	1 MSYNLIGFLQRSSNFOCQLLWQNLGRLEYCLKDRLNFIDPEIKQLQQFKEDDAALTY 60	Qy	61 EMLQNIFAIPIRDSSSTGWNNTIVENLLANYHQINHLKTYLEEKEDFTRGKLMSSL 120
Qy	61 EMLQNIFAIPIRDSSSTGWNNTIVENLLANYHQINHLKTYLEEKEDFTRGKLMSSL 120	Db	61 EMLQNIFAIPIRDSSSTGWNNTIVENLLANYHQINHLKTYLEEKEDFTRGKLMSSL 120
Db	61 EMLQNIFAIPIRDSSSTGWNNTIVENLLANYHQINHLKTYLEEKEDFTRGKLMSSL 120	Qy	121 HLKRYYGRILHYLKAKEYSCHCAWTIVRVELRNFYFINRLTGYLRN 166
Qy	121 HLKRYYGRILHYLKAKEYSCHCAWTIVRVELRNFYFINRLTGYLRN 166	Db	121 HLKRYYGRILHYLKAKEYSCHCAWTIVRVELRNFYFINRLTGYLRN 166
Db	121 HLKRYYGRILHYLKAKEYSCHCAWTIVRVELRNFYFINRLTGYLRN 166	RESULT 8	
Qy	121 HLKRYYGRILHYLKAKEYSCHCAWTIVRVELRNFYFINRLTGYLRN 166	AAB43356	AAB43356 standard; protein; 166 AA.
Db	121 HLKRYYGRILHYLKAKEYSCHCAWTIVRVELRNFYFINRLTGYLRN 166	ID	
XX		XX	
XX	DT 07-MAR-2001 (First entry)	DT	07-MAR-2001 (First entry)
XX	ID ADR83685 standard; protein; 166 AA.	XX	
XX	AC ADR83685;	DB	Human INF-beta A-chain.
AC		XX	
XX	DT 21-OCT-2004 (First entry)	KW	Interferon-beta activity; multiple sclerosis; cancer; viral infection;
XX		XX	
XX	XX	KW	
XX	XX	OS	Homo sapiens.
XX	XX	XX	
DE	Human amniotic membrane beta interferon (IFN) protein.	PN	WO200068387-A2.
XX		XX	
KW	human; amniotic membrane; beta-interferon; IFN; IFN type 1; growth;	PD	16-Nov-2000.
XX	cellular differentiation; immunoregulation.	XX	
OS	Homo sapiens.	PF	12-MAY-2000; 2000WO-US013216.
XX		XX	
PN	BR9710827-A.	PR	12-MAY-1999; 99US-0133785P.
XX		XX	

PA (XENC-) XENCOR INC.
 XX
 PI Bentzien J;
 XX
 WPI; 2001-007398/01.
 Novel interferon-beta activity (Iba) proteins which have greater stability than interferon-beta (IFN-beta) useful for the treatment of IFN -beta related disorders such as multiple sclerosis.
 Disclosure: Fig 1A; 109pp; English.

CC The present invention provides proteins which have interferon-beta (IFN-beta) activity. These analogues are produced so that they are less than 97% identical to human IFN-beta. They are useful in the treatment of multiple sclerosis, cancer, particularly osteosarcoma, basal cell carcinoma, cervical dysplasia, glioma, acute myeloid leukaemia, multiple myeloma, Hodgkin's disease, melanoma, and renal, liver and breast cancers, viral infections, including those caused by hepatitis viruses, herpes viruses and papilloma viruses, viral encephalitis, cyomegalovirus pneumonia and prophylaxis of rhinovirus, idiopathic pulmonary fibrosis and inflammatory diseases

XX Sequence 166 AA;

Query Match 100.0%; Score 874; DB 4; Length 166;
 Best Local Similarity 100.0%; Pred. No. 2, 1e-69;
 Matches 166; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 1 MSYNLIGFLQRSSNFQCKLWQNLGRLEYCLKDRMNPDIPEEIKOLQQFOKEADAALTY 60
 1 MSZNLLGFPFQRSSNFQCKLWQNLGRLEYCLKDRMNPDIPEEIKOLQQFOKEADAALTY 60

QY 61 EMLQNIAIFRQDSSSTGMNETIVENLLANYHQINHLKTIVLEEKLEKEDFTRGKLMSSL 120
 1 HLRKYYGRILHYLKAKEYSHCAWITRVEILRNFYFINRLTGYLRN 166

Db 1 MSZNLLGFPFQRSSNFQCKLWQNLGRLEYCLKDRMNPDIPEEIKOLQQFOKEADAALTY 60

QY 61 EMLQNIAIFRQDSSSTGMNETIVENLLANYHQINHLKTIVLEEKLEKEDFTRGKLMSSL 120
 1 HLRKYYGRILHYLKAKEYSHCAWITRVEILRNFYFINRLTGYLRN 166

Db 61 EMLQNIAIFRQDSSSTGMNETIVENLLANYHQINHLKTIVLEEKLEKEDFTRGKLMSSL 120

QY 121 HLRKYYGRILHYLKAKEYSHCAWITRVEILRNFYFINRLTGYLRN 166
 Db 121 HLRKYYGRILHYLKAKEYSHCAWITRVEILRNFYFINRLTGYLRN 166

RESULT 10
 AAE10346 standard; protein; 166 AA.
 ID AAE10346
 AC AAE10346;
 XX DT 10-DEC-2001 (first entry)
 XX DE Nature human beta-interferon.
 XX KW Human; beta-interferon; INF-beta; immune disease; demyelinating disease;
 KW sub-acute sclerosing panencephalomyelitis; SSeB; multiple sclerosis;
 KW metachromatic leukodystrophy; Guillain-Barre syndrome;
 KW autoimmune disease.

OS Homo sapiens.
 PN EP1133997-A2.
 XX Key Location/Qualifiers
 FT Misc-difference 162
 FT /note= "Encoded by CGT"
 XX
 DE Human INF-beta B-chain.
 XX Interferon-beta activity; multiple sclerosis; cancer; viral infection;
 KW analogue.
 XX DT 07-MAR-2001 (first entry)
 OS Homo sapiens.
 PN WO200063887-A2.
 XX PD 19-SEP-2001.
 XX
 PD 16-NOV-2000.
 XX PR 20-FEB-2001; 2001EP-00103580.
 PF 12-MAY-2000; 2000WO-US013216.
 PR 23-FEB-2000; 2000EP-00440053.
 PR 07-NOV-2000; 2000US-0246089P.
 PA (TRGE) TRANSGENE SA.
 XX PI Braun S;
 XX DR WPI; 2001-572706/65.
 XX N-PSDB; AAD17506.
 XX PT Use of nucleic acid for the treatment of immune diseases such as multiple sclerosis.

PA (XENC-) XENCOR INC.
 XX
 PI Bentzien J;
 XX
 WPI; 2001-007398/01.
 Novel interferon-beta activity (Iba) proteins which have greater stability than interferon-beta (IFN-beta) useful for the treatment of IFN

XX
PS Claim 9; Page 15; 21PP; English.
 XX
 The invention relates to use of nucleic acids expressing human beta-interferon (INF-beta) for the treatment of immune diseases such as demyelinating disease (e.g. sub-acute sclerosing panencephalomyelitis (SSPE), metachromatic leukodystrophy, Guillain-Barre syndrome) and autoimmune disease (e.g. multiple sclerosis). The expression of the beta-interferon results in the improvement of the clinical status of the treated mammal, thus avoiding the use of recombinant polypeptide. The nucleic acid is therefore compatible with the quality of life of the patients. The present sequence is mature human beta-interferon Sequence 166 AA;

Query Match 100.0%; Score 874; DB 4; Length 166;
 Best Local Similarity 100.0%; Pred. No. 2.1e-69;
 Matches 166; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 MSYNLIGFLQRSSNFFQCCQLWQLNGLEYCLKDRMNFDIPEEIKVQLQQFKEDALITY 60
 Db 1 MSYNLIGFLQRSSNFFQCCQLWQLNGLEYCLKDRMNFDIPEEIKVQLQQFKEDALITY 60
 Qy 61 EMILQNIIFAFRQDSSSTGWNETIVENLLANYHQINHLKTVLEEKLEKEDFTRGKLMSSL 120
 Db 61 EMILQNIIFAFRQDSSSTGWNETIVENLLANYHQINHLKTVLEEKLEKEDFTRGKLMSSL 120
 Qy 121 HKRYGYGRILHYLKAKEYSHCATTIVRLRNFYFINRLTGYLRN 166
 Db 121 HKRYGYGRILHYLKAKEYSHCATTIVRLRNFYFINRLTGYLRN 166

RESULT 11
 AAU00038
 ID AAU00038 standard; protein; 166 AA.
 XX
 AC AAU00038;
 XX
 DT 16-MAY-2001 (First entry)
 XX Human interferon beta.
 KW Human; interferon beta; antibody; multiple sclerosis; gene therapy;
 KW viral infection; viral hepatitis; cancer; breast cancer; inflammation;
 KW Crohn's disease; acute myeloid leukaemia; Hodgkin's disease;
 KW ulcerative colitis; immunomodulation.
 Homo sapiens.
 OS WO200115736-A2.
 XX
 PD 08-MAR-2001.
 XX
 PR 25-AUG-2000; 2000WO-DK000471.
 XX
 PR 27-AUG-1999; 99DK-00001197.
 PR 21-OCT-1999; 99US-0160732P.
 PR 26-NOV-1999; 99DK-00001691.
 PR 07-FEB-2000; 2000DK-00000194.
 PR 07-MAR-2000; 2000DK-00000363.
 PR 14-APR-2000; 2000DK-00000642.

XX
 PA (MAXY-) MAXYGEN APS.
 XX
 Pedersen AH, Schambye HT, Andersen KV, Bornaeus C, Rasmussen PB,
 XX
 PR 2001-218488/22.
 DR N-PSDB; AAS00067.
 XX
 PT A conjugate exhibiting interferon beta activity useful for treating
 PT multiple sclerosis comprises a non-polypeptide group covalently attached
 PT to an interferon beta polypeptide.
 XX

PS Example 1; Page 99-100; 108pp; English.

XX
 CC The sequence is Human interferon beta. Conjugates of the invention
 CC exhibiting interferon beta activity comprise at least one first non-
 CC polypeptide group covalently attached to an interferon beta polypeptide,
 CC the amino acid sequence of which differs from wild-type human interferon
 CC beta in at least one introduced and at least one removed amino acid
 CC residue comprising an attachment group for the first non-polypeptide
 CC group. The invention also concerns reducing the immunogenicity and/or
 CC increasing functionality in vivo half-life and/or serum half-life of an
 CC interferon beta polypeptide comprising introducing an amino acid residue
 CC constituting an attachment group for a first non-polypeptide group into a
 CC position exposed at the surface of the protein that does not contain such
 CC a group and removing an amino acid residue constituting the modified
 CC group for a first non-polypeptide group and substituting the modified
 CC peptide to conjugation with the non-polypeptide group. The conjugate and
 CC a cell culture expressing the mutated polypeptides are useful in the
 CC treatment of disease, especially multiple sclerosis, and for treating
 CC mammals having circulating antibodies against interferon beta 1a or 1b.
 CC DNA encoding the mutated proteins may be used for gene therapy. The DNA
 CC and proteins can also be used to treat viral infections (e.g. viral
 CC hepatitis), cancer (e.g. breast cancer), inflammation, Crohn's disease,
 CC acute myeloid leukaemia, Hodgkin's disease and ulcerative colitis and for
 CC immunomodulation.
 XX
 SQ Sequence 166 AA;

Query Match 100.0%; Score 874; DB 4; Length 166;
 Best Local Similarity 100.0%; Pred. No. 2.1e-69;
 Matches 166; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 MSYNLIGFLQRSSNFFQCCQLWQLNGLEYCLKDRMNFDIPEEIKVQLQQFKEDALITY 60
 Db 1 MSYNLIGFLQRSSNFFQCCQLWQLNGLEYCLKDRMNFDIPEEIKVQLQQFKEDALITY 60
 Qy 61 EMLQNIIFAFRQDSSSTGWNETIVENLLANYHQINHLKTVLEEKLEKEDFTRGKLMSSL 120
 Db 61 EMLQNIIFAFRQDSSSTGWNETIVENLLANYHQINHLKTVLEEKLEKEDFTRGKLMSSL 120
 Qy 121 HLKRYGYGRILHYLKAKEYSHCATTIVRLRNFYFINRLTGYLRN 166
 Db 121 HLKRYGYGRILHYLKAKEYSHCATTIVRLRNFYFINRLTGYLRN 166

RESULT 12

AAE11979 standard; protein; 166 AA.
 ID AAE11979;
 XX
 AC AAE11979;
 XX
 DT 18-DEC-2001 (First entry)

XX
 DE Human wild-type interferon (IFN) beta.
 XX
 KW Human; interferon-gamma; IFNG; interferon-beta; interferon alpha; FSH;
 KW follicle stimulating hormone; granulocyte colony stimulating factor;
 KW G-CSF; interleukin 10; IL-10; medicament; pulmonary administration;
 KW circulatory administration.
 XX
 Homo sapiens.
 OS
 PN WO200168141-A2.
 XX
 PD 20-SEP-2001.
 XX
 PR 16-MAR-2001; 2001WO-DK000182.
 XX
 PR 17-MAR-2000; 2000DK-00000447.
 PR 20-MAR-2000; 2000US-0190844P.
 PR 25-APR-2000; 2000WO-DK000471.
 PR 13-NOV-2000; 2000WO-DK000631.
 XX
 PA (MAXY-) MAXYGEN APS.

XX Hansen CK;
 PI -
 XX WPI: 2001-616274/71.
 XX **Dispersions of particles for administration to the lung and circulatory system by inhalation, e.g. from a nebulizer.**
 XX **Claim 22:** Page 136; 139pp; English.
 XX The present invention relates to novel dispersions of a conjugate comprising at least one non-polypeptide moiety covalently attached to a polypeptide variant, wherein the amino acid sequence of the polypeptide variant differs from that of the corresponding wild-type human polypeptide in that at least 1 residue comprising an attachment group for the non-polypeptide group has been introduced and/or removed. The wild-type human polypeptide group is selected from the group consisting of interferon-gamma (IFNG), interferon beta, interferon alpha, follicle stimulating hormone, (FSH), interleukin 10 (IL-10) and granulocyte colony stimulating factor (G-CSF). The dispersion is used for the preparation of a medicament for pulmonary and/or circulatory administration. The present sequence is human wild type interferon (IFN) beta
 XX Sequence 166 AA;
 Query Match 100.0%; Score 874; DB 4; Length 166;
 Best Local Similarity 100.0%; Pred. No. 2_1e-69;
 Matches 166; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 MSYNLIGFLQRSSNFOCQKLWQNLGRLEYCLKDRMNPDIPEEKIQLQQFQKEADAALTY 60
 Db 1 MSYNLIGFLQRSSNFOCQKLWQNLGRLEYCLKDRMNPDIPEEKIQLQQFQKEADAALTY 60
 Qy 61 EMLQNIAFPDQSSTGMNETVNLLANVYHQINHLKVLEEKLEKDFTRGKLMSSL 120
 Db 61 EMLQNIAFPDQSSTGMNETVNLLANVYHQINHLKVLEEKLEKDFTRGKLMSSL 120
 Qy 121 HLKRYYGRILHYLAKKEYSHCAWTIVRVEILRNFYFINRLTGYLRN 166
 Db 121 HLKRYYGRILHYLAKKEYSHCAWTIVRVEILRNFYFINRLTGYLRN 166
 RESULT 14
 ABG97960
 ID ABG97960 standard; protein; 166 AA.
 XX AC ABG97960;
 XX DT 07-JAN-2003 (first entry)
 DE Human interferon beta (INFBeta) wild-type protein.
 XX KW Human; interferon beta; INFBeta; non-immunogenic; T-cell epitope;
 KW major histocompatibility complex; MHC class II ligand; MHC allele;
 KW reduced immunogenicity.
 XX OS Homo sapiens.
 XX PR WO200274783-A2.
 XX PD 26-SEP-2002.
 XX PF 15-MAR-2002; 2002WO-EP002925.
 XX PR 15-MAR-2001; 2001EP-0016539.
 XX PA (MERCK) MERCK PATENT GMBH.
 XX PI Carr FU, Carter G, Jones T, Watkins J, Baker M;
 XX DR WPI; 2002-750532/81.
 XX PT New modified molecule with the biological activity of human interferon (INF) beta that is non-immunogenic or less immunogenic than any non-modified molecule, useful for vaccination to reduce immunogenicity to INF beta in vivo.
 XX PT
 XX PS Disclosure; Page 5; 60pp; English.
 XX DR WPI; 2002-121134/16.

XX Nuclic acid molecules encoding interferon epsilon polypeptides useful for treating certain autoimmune diseases, cancers and for the enhancement of immune response against infectious agents.
 XX PT
 PT
 PS Disclosure; Fig 1; 59pp; English.
 XX CC The invention relates to an isolated nucleic acid molecule encoding a murine interferon epsilon (IFN-epsilon, Zifine) polypeptide. IFN-epsilon DNA is useful for producing IFN-epsilon polypeptides which is useful for treating autoimmune diseases, cancers, tumours and lymphoproliferative disorders including B-cell lymphoma, chronic lymphatic leukaemia and acute lymphatic leukaemia. IFN-epsilon protein is useful for the enhancement of immune response against infectious agents e.g. virus. IFN-epsilon DNA is useful in gene therapy. The present sequence is human interferon (IFN)-beta protein
 XX SQ Sequence 166 AA;
 Query Match 100.0%; Score 874; DB 5; Length 166;
 Best Local Similarity 100.0%; Pred. No. 2_1e-69;
 Matches 166; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 MSYNLIGFLQRSSNFOCQKLWQNLGRLEYCLKDRMNPDIPEEKIQLQQFQKEADAALTY 60
 Db 1 MSYNLIGFLQRSSNFOCQKLWQNLGRLEYCLKDRMNPDIPEEKIQLQQFQKEADAALTY 60
 RESULT 14
 ABG97960
 ID ABG97960 standard; protein; 166 AA.
 XX AC ABG97960;
 XX DT 07-JAN-2003 (first entry)
 DE Human interferon beta (INFBeta) wild-type protein.
 XX KW Human; interferon beta; INFBeta; non-immunogenic; T-cell epitope;
 KW major histocompatibility complex; MHC class II ligand; MHC allele;
 KW reduced immunogenicity.
 XX OS Homo sapiens.
 XX PR WO200274783-A2.
 XX PD 26-SEP-2002.
 XX PF 15-MAR-2002; 2002WO-EP002925.
 XX PR 15-MAR-2001; 2001EP-0016539.
 XX PA (MERCK) MERCK PATENT GMBH.
 XX PI Carr FU, Carter G, Jones T, Watkins J, Baker M;
 XX DR WPI; 2002-750532/81.
 XX PT New modified molecule with the biological activity of human interferon (INF) beta that is non-immunogenic or less immunogenic than any non-modified molecule, useful for vaccination to reduce immunogenicity to INF beta in vivo.
 XX PT
 XX PS Disclosure; Page 5; 60pp; English.
 XX DR WPI; 2002-121134/16.

A;Residues: 1-68 <HO2>
A;Cross-references: UNIPARC:UPI0000173664
R;Wetzel, R.; 606-607, 1981
A;Title: Assignment of the disulfide bonds of leukocyte interferon.
A;Reference number: A93244; MUID:81123083; PMID:6162107
A;Contents: annotation; disulfide bond
R;Shepard, H. M.; Leung, D.; Stebbing, N.; Goeddel, D. V.
Nature 289, 562-565, 1981
A;Title: A single amino acid change in IFN-beta-1 abolishes its antiviral activity.
A;Reference number: A93269; MUID:82080683; PMID:6171735
A;Molecule type: mRNA
A;Residues: 71-161, 'Y', 163-187 <SHE>
A;Cross-references: UNIPARC:UPI000173665
A;Experimental source: variant, clone pF516
A;Note: the loss of Cys-162 (and of the ability to form the essential disulfide bond) in R;Utsunomi, J.; Mizuno, Y.; Hosoi, K.; Okano, K.; Sawada, R.; Kajitani, M.; Sakai, I.; Nar Bur. J. Biochem. 181, 545-553, 1989
A;Title: Characterization of four different mammalian-cell-derived recombinant human int A;Accession: S04479; MUID:89276336; PMID:2731537
A;Accession: S04479; MUID:89276336; PMID:2731537
A;Status: preliminary
A;Molecule type: Protein
A;Residues: 22-187 <UTS>
A;Cross-references: UNIPARC:UPI000002BE76
R;May, L.T.; Seigal, P.B.
J. Interferon Res. 5, 521-526, 1985
A;Title: On the relationship between human interferon alpha-1 and beta-1 genes.
A;Reference number: I56315; MUID:86035565; PMID:2414376
A;Accession: I56315
A;Status: preliminary; translated from GB/EMBL/DDJB
A;Molecule type: mRNA
A;Residues: 1-187 <UTM>
A;Cross-references: UNIPARC:UPI00004775D; GB:M28622; NID:g184624; PIDN:AAA36040.1; PID: C;Genetics
A;Gene: GDB:IFNB1; IFNB
A;Cross-references: GDB:120522; OMIM:147640
A;Map Position: 9p21-9p21
C;Superfamily: interferon alpha
C;Keywords: antiviral
F;1-21/Domain: signal sequence #status predicted <SIG>
F;22-187/Product: interferon beta-1 #status experimental <MAT>
F;52-162/Disulfide bonds: #status predicted
Query Match Score 100.0%; Best Local Similarity 100.0%; Pred. No. 5.6e-4; Matches 166; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 MSYNLGLPQRSSNFQCCQLLWOLNGRLYECLKDRMNFDIPEIKLQQFOKEADAALITY 60
Db 22 MSNLGLGFQRSSNFQCCQLLWOLNGRLYECLKDRMNFDIPEIKLQQFOKEADAALITY 81
Qy 61 EMLQNIIFAFRQDSSTGWNETIVENILANYHQINHLKTIVLEEKLEDFTRGKLMSSL 120
Db 82 EMLQNIIFAFRQDSSTGWNETIVENILANYHQINHLKTIVLEEKLEDFTRGKLMSSL 141
Qy 121 HKRYYGRILHYLAKKEYSHCAWTIVRLNRYFIRNLTYGLRN 166
Db 142 HKRYYGRILHYLAKKEYSHCAWTIVRLNRYFIRNLTYGLRN 187

RESULT 2
IVBOB2
Interferon beta-2 precursor - bovine
C;Species: Bos primigenius taurus (cattle)
C;Date: 15-Nov-1984 #sequence_revision 15-Nov-1984 #text_change 09-Jul-2004
C;Accession: A01840
R;Leung, D.W.; Capon, D.J.; Goeddel, D.V.
Bio/Technology 2, 458-464, 1984
A;Title: The structure and bacterial expression of three distinct bovine interferon-beta
A;Reference number: A90097
A;Accession: A01840

A;Molecule type: DNA
A;Residues: 1-186 <LEU>
A;Cross-references: UNIPROT:D01576; UNIPARC:UPI000012D64C
C;Superfamily: interferon alpha
C;Keywords: Glycoprotein
F;1-21/Domain: signal sequence #status predicted <SIG>
F;22-186/Product: interferon beta-2 #status predicted
F;52-161/Disulfide bonds: #status predicted
F;131,173/Binding site: carbohydrate (Asn) (covalent) #status predicted
Query Match Score 56.4%; Best Local Similarity 57.9%; Matches 95; Conservative 30; Mismatches 38; Indels 1; Gaps 1;
Qy 2 SYNLLGLPQSSNFQCCQLLWOLNGRLYECLKDRMNFDIPEIKLQQFOKEADAALITY 61
Db 23 SYSLRFQRSRSLALCQKLRLQPLSPPOHCLEARNDFQMBEMKQAAQFOKEADAALITY 82
Qy 62 MLQNITAIIFRQDSSTGWNETIVENILANYHQINHLKTIVLEEKLEDFTRGKLMSSLH 121
Db 83 MLQQTINILPFLPQDFSSGWSSETTILEEYEQMHNLEPQKEIQMKQNSTMGD-TTVLRH 141
Qy 122 LRKYYGRILHYLAKKEYSHCAWTIVRLNRYFIRNLTYGLRN 165
Db 142 LRKYYFNLVQYLKSKEYNRCAWTIVRLNFSFLTRLYGLRN 185

RESULT 3
IVBOB1
Interferon beta-1 precursor - horse
N;Alternate names: EqIFN-beta-1; type I interferon
C;Species: Equus caballus (domestic horse)
C;Date: 28-Dec-1987 #sequence_revision 28-Dec-1987 #text_change 09-Jul-2004
C;Accession: G24912
R;Himmler, A.; Hauptmann, R.; Adolf, G.R.; Swetly, P.
DNA 5, 345-356, 1986
A;Title: Molecular cloning and expression in Escherichia coli of equine type I interferon
A;Reference number: A90956; MUID:87053170; PMID:302999
A;Accession: G24912
A;Molecule type: mRNA
A;Cross-references: UNIPROT:P05012; UNIPARC:UPI000002C9FB; GB:M14546; NID:9164228; PIDN:
C;Superfamily: interferon alpha
C;Keywords: antiviral; glycoprotein
F;1-21/Domain: signal sequence #status predicted <SIG>
F;22-186/Product: interferon beta-1 #status predicted
F;101,136/Binding site: carbohydrate (Asn) (covalent) #status predicted
Query Match Score 55.8%; Best Local Similarity 59.0%; Matches 27; Mismatches 40; Indels 1; Gaps 1;
Qy 1 MSYNLGLPQSSNFQCCQLLWOLNGRLYECLKDRMNFDIPEIKLQQFOKEADAALITY 60
Db 22 VNYDLRSQQRSSNSACMLIRQNLGAPQRCPEDTMNFQYQPEIEAQAFQKEADAALITY 81
Qy 61 EMLQNIIFAFRQDSSTGWNETIVENILANYHQINHLKTIVLEEKLEDFTRGKLMSSL 120
Db 82 EMLQNIIFAFRQDSSTGWNETIVENILANYHQINHLKTIVLEEKLEDFTRGKLMSSL 141
Qy 121 HKRYYGRILHYLAKKEYSHCAWTIVRLNRYFIRNLTYGLRN 166
Db 141 RLKYYGRISOLYKAKCYSHCAWTIVRLNRYFIRNLTYGLRN 186

RESULT 4
IVBOB3
Interferon beta-3 precursor - bovine
C;Species: Bos primigenius taurus (cattle)
C;Date: 15-Nov-1984 #sequence_revision 15-Nov-1984 #text_change 09-Jul-2004
C;Accession: A01841
R;Leung, D.W.; Capon, D.J.; Goeddel, D.V.
Bio/Technology 2, 458-464, 1984
A;Title: The structure and bacterial expression of three distinct bovine interferon-beta
A;Reference number: A90097
A;Accession: Bio/Technology 2, 458-464, 1984

A;Title: The structure and bacterial expression of three distinct bovine interferon-beta
A;Reference number: A90097
A;Accession: A01841
A;Molecule type: DNA
A;Residues: 1-186 <LEU>
A;Cross-references: UNIPROT:PO1577; UNIPARC:UPI000012D64E
C;Superfamily: interferon alpha
C;Keywords: glycoprotein
P;1-21/Domain: signal sequence #status predicted <SIG>
F;22-186/Product: interferon beta-3 #status predicted <MAT>
F;52-161/Disulfide bonds: #status predicted
P;131,173/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match Score 458.5%; DB 1; Length 186;
Best Local Similarity 53.3%; Pred. No. 3e-30; Indels 1; Gaps 1;
Matches 88; Conservative 35; Mismatches 41; Indels 1; Gaps 1;
A;Residues: 1-182 <KUG>
A;Cross-references: UNIPARC:UPI000022EE3; EMBL:X14028; PIDN:951550; PIDN:
R;Vodjdan, G.; Coulombe, C.; Doy, J.
J. Mol. Biol. 204, 221-231, 1988

A;Title: Structure and characterization of a murine chromosomal fragment containing the i
A;Reference number: S02020; PMID:3221389
A;Accession: S02020
A;Molecule type: DNA
A;Residues: 1-182 <VOD>
A;Cross-references: UNIPROT:PO1575; UNIPARC:UPI000022EE3; EMBL:X14028; PIDN:
R;Kuga, T.; Fujita, T.; Taniguchi, T.
Nucleic Acids Res. 17, 3291, 1989

A;Title: Nucleotide sequence of the mouse interferon-beta gene.
A;Reference number: S04201; PMID:8926375; PMID:2726460
A;Accession: S04201
A;Status: translation not shown
A;Molecule type: DNA
A;Residues: 1-182 <KUG>
A;Cross-references: UNIPARC:UPI000022EE3; EMBL:X14455; PIDN:951538; PIDN:
R;Higashi, Y.; Sokawa, Y.; Kawade, Y.; Ohno, S.; Takaoka, C.; Taniguchi, T.
J. Biol. Chem. 258, 9522-9529, 1983

A;Title: Structure and expression of a cloned cDNA for mouse interferon-beta.
A;Reference number: A01839; PMID:83265757; PMID:6888252
A;Accession: A01839
A;Molecule type: mRNA
A;Residues: 1-182 <HIG>
A;Cross-references: UNIPARC:UPI000022EE3; GB:K00020; PIDN:9194113; PIDN:
C;Genetics:

Query Match Score 458.5%; DB 1; Length 186;
Best Local Similarity 53.3%; Pred. No. 3e-30; Indels 1; Gaps 1;
Matches 88; Conservative 35; Mismatches 41; Indels 1; Gaps 1;
A;Map position: 4
C;Keywords: Glycoprotein
C;Superfamily: interferon alpha
F;1-21/Domain: signal sequence #status predicted <MAT>
F;22-182/Product: interferon beta #status predicted <MAT>
F;50, 90, 97/Binding site: carboxyhydride (Asn) (covalent) #status predicted

RESULT 5
IVBOB1
interferon beta-1 precursor - bovine
C;Species: Bos primigenius taurus (cattle)
C;Date: 15-Nov-1984 #sequence_revision 15-Nov-1984 #text_change 09-Jul-2004
C;Accession: A01842
R;Leung, D.W.; Capon, D.J.; Goeddel, D.V.
BIC/Technology 2, 458-464, 1984
A;Title: The structure and bacterial expression of three distinct bovine interferon-beta
A;Reference number: A90097
A;Accession: A01842
A;Molecule type: DNA
A;Residues: 1-186 <LEU>
A;Cross-references: UNIPROT:PO1578; UNIPARC:UPI000012D64B
C;Keywords: glycoprotein
C;Superfamily: interferon alpha
P;1-21/Domain: signal sequence #status predicted <SIG>
F;22-186/Product: interferon beta-1 #status predicted <MAT>
F;52-161/Disulfide bonds: #status predicted
P;131,173/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match Score 440.5%; DB 1; Length 186;
Best Local Similarity 51.5%; Pred. No. 8.6e-29; Indels 1; Gaps 1;
Matches 85; Conservative 36; Mismatches 43; Indels 1; Gaps 1;
A;Residues: 1-184 <YOK>
A;Cross-references: UNIPROT:PO1575; UNIPARC:UPI000022EE3; EMBL:X14028; PIDN:
R;Yokoyama, S.; Oishi, N.; Shamoto, M.; Watanabe, Y.; Yagi, K.
Biophys. Res. Commun. 232, 698-701, 1997

A;Title: Isolation and expression of rat interferon beta gene and growth-inhibitory effect
A;Reference number: JC5424; PMID:97271387; PMID:9126338
A;Accession: JC5424
A;Molecule type: DNA
A;Residues: 1-184 <YOK>
A;Cross-references: UNIPROT:PO70499; UNIPARC:UPI00012D652; DBP:D87919; PIDN:91616938; PI
C;Comment: This protein exhibits characteristic antiviral and antitumor activities.
C;Genetics:

Query Match Score 335.5%; DB 2; Length 184;
C;Superfamily: interferon alpha
F;1-21/Domain: signal sequence #status predicted <SIG>
F;22-184/Product: interferon beta #status predicted <MAT>

RESULT 6
IVMSB
interferon beta precursor - mouse
C;Species: Mus musculus (house mouse)
C;Date: 03-Aug-1984 #sequence_revision 03-Aug-1984 #text_change 09-Jul-2004

Best Local Similarity 45.8%; Pred. No. 2.8e-20; Matches 76; Conservative 24; Mismatches 63; Indels 3; Gaps 2;

Qy 1 MSYNLGFLQRSSNFQCOKLWQLNGRLYCLKDRAFNFDIPEIKQLQQFQEKAEDALTIY 60
Db 22 IDYKQLOFRQSTSIRTCKLQLFQLNGLN--LSYRDFKIPMEVMPQSOMEKSYTAFAIQ 79

Qy 61 EMQNQFAIFRQDSSSTGWNETIVENILANVHQINHLKTYLEEKLEKEDFTRGKLMSS 120
Db 80 VNLQNVLFVRSNTSSTGWNETIVESLDEHQQTEILETKEK-QUEERLTWTSITTL 138

Qy 121 HKRYGYGRILHYLKAKEYSHCAWTIVRLRNFYEFINRLGYLNR 166

Db 139 GLKSYYNRVQYIKDKKYNNSVAMMUVRAEVPNFSSTILRNLRNRFQ 184

RESULT 8
IVHO22
interferon alpha-II-2 precursor - horse
C;Species: Equus caballus (domestic horse)
C;Date: 28-Dec-1987 #sequence_revision 28-Dec-1987 #text_change 09-Jul-2004
R;Himmller, A.; Hauptmann, R.; Adolf, G.R.; Swetly, P.
DNA 5, 345-356, 1986
A;Title: Molecular cloning and expression in Escherichia coli of equine type I interferon
A;Reference number: A90956; MUID:87053170; PMID:3022999
A;Accession: F24912
A;Molecule type: DNA
A;Residues: 1-195 <HIM>
A;Cross-references: UNIPROT:P05002; UNIPARC:UPI000002CA65; GB:M14545; NID:9164217; PIDN:
C;Superfamily: interferon alpha
C;Keywords: antiviral, glycoprotein
F,1-23/Domain: signal sequence #status predicted <SIG>
F,24-195/Product: interferon alpha-II-2 #status predicted <MAT>
F,24-122,52-162/Disulfide bonds: #status predicted
F,101/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match Score 289; DB 1; Length 195;
Best Local Similarity 37.2%; Pred. No. 1.8e-16;
Matches 61; Conservative 33; Mismatches 56; Indels 14; Gaps 1;

Qy 2 SYNLIGFLQRSSNFQCOKLWQLNGRLYCLKDRAFNFDIPEIKQLQQFQEKAEDALTIY 61
Db 37 NLQIGMQRSS-----AICLKDRKOFREFQDMADPQFPAQASVLIHE 82

Qy 62 MQNQFAIFRQDSSSTGWNETIVENILANVHQINHLKTYLEEKLEKEDFTRGKLMSS 121
Db 83 MlQOQISLHTERSAAWNNTILEDELTGLLRLQEDLDTCQEMGEESALGTVRPTLA 142

Qy 122 HKRYGYGRILHYLKAKEYSHCAWTIVRLRNFYEFINRLGYLNR 166
Db 143 VKRYFRGITHLYLKEXKYSDCAWEVNEMRSFSSSANLQRLR 186

RESULT 9
IVHO21
interferon alpha-II-1 precursor - horse
C;Species: Equus caballus (domestic horse)
C;Date: 28-Dec-1987 #sequence_revision 28-Dec-1987 #text_change 09-Jul-2004
R;Himmller, A.; Hauptmann, R.; Adolf, G.R.; Swetly, P.
DNA 5, 345-356, 1986
A;Title: Molecular cloning and expression in Escherichia coli of equine type I interferon
A;Reference number: A90956; MUID:87053170; PMID:3022999
A;Accession: F24912
A;Molecule type: DNA
A;Residues: 1-195 <HIM>
A;Cross-references: UNIPROT:P05001; UNIPARC:UPI000002CA9FC; GB:M14544; NID:9164230; PIDN:
C;Superfamily: interferon alpha
C;Keywords: antiviral, Glycoprotein
F,1-23/Domain: signal sequence #status predicted <SIG>

F,24-195/Product: interferon alpha-II-1 #status predicted <MAT>
F,24-122,52-162/Disulfide bonds: #status predicted
F,101/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match Score 268; DB 1; Length 195;
Best Local Similarity 41.0%; Pred. No. 9.1e-15;
Matches 55; Conservative 29; Mismatches 53; Indels 0; Gaps 0;

Qy 31 CLKDRMFNPDEBIRKQLQQFQEKAEDALTIYEMQNQFAIFRQDSSSTGWNETIVENILAN 90
Db 52 CLKHRTDFRPFQEQLDGPQEPAQTSVLQEMLQOIVSLFHTERSAAWNNTLIDRLLAG 111

Qy 91 VYHQINHLKTYLEEKLEKEDFTRGKLMSSHLKRYGYGRILHYLKAKEYSHCAWTIVRL 150
Db 112 LHQQLEDDLNTCLDEQFEEBSALGTIVGPTLVKRYFRRFLYLTETKYSDCAWEVTVVDI 171

Qy 151 LRNFYFIRNRLTGYL 164
Db 172 MRSFSSSANLQRL 185

RESULT 10
IVHOA1
interferon alpha-I-1 precursor - horse
C;Alternate names: EqIFN-alpha-I-1; type I interferon
C;Species: Equus caballus (domestic horse)
C;Accession: A24912
C;Date: 28-Dec-1987 #sequence_revision 28-Dec-1987 #text_change 09-Jul-2004
R;Himmller, A.; Hauptmann, R.; Adolf, G.R.; Swetly, P.
DNA 5, 345-356, 1986
A;Title: Molecular cloning and expression in Escherichia coli of equine type I interferon
A;Reference number: A90956; MUID:87053170; PMID:3022999
A;Accession: F24912
A;Molecule type: DNA
A;Residues: 1-184 <HIM>
A;Cross-references: UNIPROT:P05003; UNIPARC:UPI000002C9F9; GB:M14540; NID:9164226; PIDN:
C;Superfamily: interferon alpha
C;Keywords: antiviral
F,1-23/Domain: signal sequence #status predicted <SIG>
F,24-184/Product: interferon alpha-I-1 #status predicted <MAT>
F,24-122,52-162/Disulfide bonds: #status predicted
F,101/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match Score 264; DB 1; Length 184;
Best Local Similarity 36.7%; Pred. No. 1.8e-14;
Matches 55; Conservative 29; Mismatches 52; Indels 14; Gaps 1;

Qy 5 LLGFQRSNNFQCKLWLQNLGRLEYCLKDRAFNFDIPEIKQLQQFQEKAEDALTYEMLQ 64
Db 40 LLGQMRIRISPPS-----CLDRNDFGFPQEYFDGQNRKPQQAISAVHETIQ 85

Qy 65 NIFAFRQDSSSTGWNETIVENILANVHQINHLKTYLEEKLEKEDFTRGKLMSSHLKR 124
Db 86 QIFHFISTDSESSAAADESLLDKLTGLYQOLTEACLSOBGVETPLMNEDSSLAVRR 145

Qy 125 YYGRILHYLKAKEYSHCAWTIVRLRNFYEFINRLGYLNR 154
Db 146 YFQIALYQEKKYSPCAWEVRAIMRSP 175

RESULT 11
IVHOA3
interferon alpha-I-3 precursor - horse
C;Alternate names: EqIFN-alpha-I-3; type I interferon
C;Species: Equus caballus (domestic horse)
C;Accession: C24912
C;Date: 28-Dec-1987 #sequence_revision 28-Dec-1987 #text_change 09-Jul-2004
R;Himmller, A.; Hauptmann, R.; Adolf, G.R.; Swetly, P.
DNA 5, 345-356, 1986
A;Reference number: A90956; MUID:87053170; PMID:3022999
A;Accession: F24912
A;Molecule type: DNA
A;Residues: 1-184 <HIM>
A;Cross-references: UNIPROT:P05001; UNIPARC:UPI000002CA9FC; GB:M14544; NID:9164230; PIDN:
C;Superfamily: interferon alpha
C;Keywords: antiviral, Glycoprotein
F,1-23/Domain: signal sequence #status predicted <SIG>

Db 40 LIAQM-GRISHESCLKDRYDFGFQPEVFDGNGQFQKAQAIASFHEMIQQTFNLSTKDSSA 98
 Qy 78 GWNNTIVENLLANVHQLINHKLTKVLEEKLEKEDDFTRGKLMASLHKRYIGRILHLKARE 137
 Db 99 AWEDETLIDKFKYIELFQQLNDLEACVTCQEVGVEIAALMNEEDSILAVRKYFQRITLYLMGKK 158
 Qy 138 YSHCANTIVRVEILRNYYFINRLTGYL 165
 Db 159 YSPCAWEVRABIMRSFSPTNLQKCLR 186

RESULT 15
 IVHOA2
 interferon alpha-1-2 precursor - horse
 N;Alternate names: Equine alpha-I-2, type I interferon
 C;Species: *Bos taurus* (domestic horse)
 C;Date: 28-Dec-1987 #sequence_revision 28-Dec-1987 #text_change 09-Jul-2004
 C;Accession: B24912
 R;Himmiller, A.; Hauptmann, R.; Adolf, G.R.; Swetly, P.
 A;Title: Molecular cloning and expression in *Escherichia coli* of equine type I interferon
 A;Reference number: A90956; MUID:87053170; PMID:3022999
 A;Cross-references: UNIPROT:PO5004; UNIPARC:UPI000002C9FA; GB:MA4541; NID:9164218; FIDN:
 C;Superfamily: interferon alpha
 C;Keywords: antiviral
 F;1-23/Domain: signal sequence #status predicted <SIG>
 F;24-184/Product: interferon alpha-1-2 #status predicted <MAT>
 F;24-184/24-122,52-162/Disulfide bonds: #status predicted

Query Match Score 29.7%; Score 260; DB 1; Length 184;
 Best Local Similarity 36.7%; Pred. No. 3.8e-14;
 Matches 55; Conservative 28; Mismatches 53; Indels 14; Gaps 1;

Qy 5 LIGFLQSSNFQQKLWQLQNLGRLEYCLDKRMNFDPPEKOLQOFQKEDDALTYEMLQ 64
 Db 40 LIGQMRPISPFs-----CLKDNDFGPQEVDGNGQPRKEPAISAVHETIQ 85
 Qy 65 NIFAIFFRQDSSSTGMNETTIVENLLANYHQINHLKTVLEEKEDFTRGKLMSSLHLK 124
 Db 86 QIFHLFSTDGSAAWDSLDDLYQQLTEACLSQEYGVETPLMNEEDSLLAVRR 145
 Qy 125 YYGRILHYLAKAEYSHGCAWTIVRVEILRNF 154
 Db 146 YFQRIALYQERKYSPCAWEIVRAEIMRCF 175

Search completed: December 21, 2005, 14:17:48
 Job time : 39 secs